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Scientific and Technical Information Center

### SEARCH REQUEST FORM

Date: 1/10/00 Requester's Full Name: \_\_\_\_\_ Examiner #: Lil Lee  
Art Unit: 1645 Phone (308) 8891 Serial Number: 09/041,236  
Results Format Preferred (circle): PAPER DISK E-MAIL

\*\*\*\*\*  
To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Date: \_\_\_\_\_

**Search Topic:**

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, grandchild, divisional, or issued patent numbers) along with the appropriate serial number.

please search =

R. NO INVENTION AA AA AA AA  
(NA)

Back translate SEQ ID NO: 2 into NA and run against NA database  
(AA)

RECEIVED

JAN 10 2000

STIC  
TECH/CHEM. DIVISION

Point of Contact:  
Susan Hanley  
Technical Info. Specialist  
CM1 12C14 Tel: 305-4053

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Searcher: \_\_\_\_\_

Searcher Phone #: \_\_\_\_\_

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: \_\_\_\_\_

Date Completed: \_\_\_\_\_

Searcher Prep & Review Time: \_\_\_\_\_

Online Time: \_\_\_\_\_

**Type of Search**

\_\_\_\_ NA Sequence (#)

\_\_\_\_ AA Sequence (#)

\_\_\_\_ Structure (#)

\_\_\_\_ Bibliographic

\_\_\_\_ Litigation

\_\_\_\_ Fulltext

\_\_\_\_ Other

**Vendors and Cost**

\_\_\_\_ STN \_\_\_\_\_ Dialog

\_\_\_\_ Questel/Orbit \_\_\_\_\_ Dr.Link

\_\_\_\_ Lexis/Nexis \_\_\_\_\_ Westlaw

\_\_\_\_ WWW/Internet

\_\_\_\_ In-house sequence systems (list)

\_\_\_\_ Other (specify)

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REFERENCE
AUTHORS Yamada, A., Kubo, K., Takeshita, T., Harashima, N., Kawano, K., Mine, T.,
Sagawa, K., Sugamura, K. and Itoh, K.
TITLE Molecular cloning of a glycosylphosphatidylinositol-anchored
molecule CDw108
JOURNAL J. Immunol. 162 (7), 4094-4100 (1999)
MEDLINE 99219431
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AUTHORS Yamada, A., Kubo, K., Takeshita, T., Harashima, N., Kawano, K.,
Sagawa, K., Sugamura, K. and Itoh, K.
Direct Submission
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JOURNAL Submitted (02-JUN-1998) Immunology, Kurume University School of
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AUTHORS Xu,X., Ng,S., Wu,Z.L., Nguyen,D., Homburger,S., Seidel-Dugan,C.,
Ebens,A. and Luo,Y.
Human semaphorin K1 is glycosylphosphatidylinositol-linked and
defines a new subfamily of viral-related semaphorins
J. Biol. Chem. 273 (35), 22428-22434 [1998]
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REFERENCE 2 (bases 1 to 2594)
AUTHORS Xu,X. and Luo,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1998) Biology, Exelixis Pharmaceuticals, Inc., 260
Littlefield Ave., South San Francisco, CA 94080, USA
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AUTHORS	1 (sites)		
TITLE	Sato, Y. and Takahashi, H.		
JOURNAL	Molecular cloning and expression of novel Semaphorin family molecule		
REFERENCE	Unpublished (1998)		
AUTHORS	2 (bases 1 to 2608)		
TITLE	Takahashi, H. and Sato, Y.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (08-SEP-1998) to the DDBJ/EMBL/GenBank databases. H		
AUTHORS	Takahashi, Mitsubishi Kasei Institute of Life Sciences,		
TITLE			
JOURNAL			

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AUTHORS Mine,T., Harada,K., Matsumoto,T., Yamana,H., Itoh,K. and Yamada,A.  
TITLE CDw108 expression during T-cell development  
JOURNAL Unpublished



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REFERENCE
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AUTHORS Lange, C., Liehr, T., Goen, M., Gebhart, E., Fleckenstein, B. and

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Ensser, A.
New eukaryotic semaphorins with close homology to semaphorins of
DNA viruses
Genomics 51 (3), 340-350 (1998)
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AUTHORS Ensser, A., Liehr, T., Lange, C., Goen, M., Gebhart, E. and
Fleckenstein, B.
Direct submission
Submitted (22-OCT-1997) Institut fuer Klinische und Molekulare
Virologie, Friedrich Alexander Universitaet, Schlossgarten 4,
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ACCESSION  U18243
VERSION    g1000716
KEYWORDS   U18243.1 GI:1000716
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            Enser A. and Fleckenstein B.
            Alcelaphine herpesvirus type 1 has a semaphorin-like gene
            J. Gen. Virol. 76 (Pt 4), 1063-1067 (1995)
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            Direct Submission
            Enser A.
            Submitted (07-DEC-1994) Armin Enser, Institut fuer Virologie,
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ACCESSION AR040598
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VERSION AR040598.1 GI:5959961
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ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2601)
AUTHORS Goodman,C.S., Kolodkin,A.L., Matthes,D., Bentley,D.R. and O'Connor,T.
TITLE Semaphorin gene family
JOURNAL Patent: US 5807826-A 53 15-SEP-1998;
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seq\_documentation\_block:

LOCUS HUMHEM 2530 bp mRNA PRI 08-MAY-1995  
DEFINITION Homo sapiens semaphorin-III (Hsema-III) mRNA, complete cds.

ACCESSION L26081

NID 9799328

VERSION L26081.1 GI:799328

KEYWORDS semaphorin.

SOURCE Homo sapiens (human).

ORGANISM Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 2530)

AUTHORS Kolodkin,A.L., Matthes,D.J. and Goodman,C.S.

TITLE The semaphorin genes encode a family of transmembrane and secreted  
growth cone guidance molecules

JOURNAL Cell 75 (7), 1389-1399 (1993)

MEDLINE 94094332

COMMENT On May 8, 1995 this sequence version replaced gi:436559.

FEATURES

Location/Qualifiers

1..2530

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/db\_xref="taxon:9606"

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/tissue\_type="brain"

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/gene="Hsema-III"

16..2331

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BASE COUNT 786 a 518 c 576 g 650 t

ORIGIN

alignment\_scores:

Quality: 649.50 Length: 687

Ratio: 1.620 Gaps: 27

Percent Similarity: 58.370 Percent Identity: 28.093

alignment\_block:

US-09-041-236-2 x HUMHEM

Alignment seg 1/1 to: HUMHEM from: 1 to: 2530

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1564 GGCACAGCTTCTTACACCGCTGTGACATCTATGGCAAGCCGTGTGCAG 1613
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1614 AATGCTGCTCGCTCGGAGCCCTTACTGTGCTGGGATGGTCTCATGC 1663
487 lIleSerileTy.....SerSerGluArgSerValLeuGlnSerIleAs 501
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559 isGlnSerProAsnCysIle.....LeuPheIleGluAsn 570
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seq\_name: gb\_ro:MWRNASEMA

seq\_documentation\_block:

LOCUS MWRNASEMA 2872 bp mRNA ROD 08-JUL-1996  
DEFINITION M.musculus mRNA for semaphorin A.  
ACCESSION X85990  
NID 9854323  
VERSION X85990.1 GI:854323  
KEYWORDS sema gene; semaphorin.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 2872)  
AUTHORS Puschel, A.W., Adams, R.H. and Betz, H.  
TITLE Murine semaphorin D/collapsin is a member of a diverse gene family  
and creates domains inhibitory for axonal extension  
JOURNAL Neuron 14 (5), 941-948 (1995)  
MEDLINE 95267431  
REFERENCE 2 (bases 1 to 2872)  
AUTHORS Adams, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (30-MAR-1995) R.H. Adams, Max-Planck-Institute fuer  
Hirnforschung, Deutscherstr. 46, D- 60528 Frankfurt, FRG  
COMMENT Sequence overlapping with those under the acc#U02528, L26080,  
L26081 & L26082.

FEATURES  
Location/Qualifiers  
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BASE COUNT 592 a 799 c 882 g 599 t  
ORIGIN

alignment\_scores:

Quality: 634.50

Ratio: 1.571

Percent Similarity: 54.083

Length: 747

Gaps: 27

Percent Identity: 27.443

alignment\_block:

US-09-041-236-2 x MWRNASEMA

Align seg 1/1 to: MWRNASEMA from: 1 to: 2872

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584 InGluGlySerTyrPheArgGluAlaGlnHisTrpGlnLeuLeuProGlu 600  
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601 AspGlyIleMetAlaGluHisLeuLeuGlyHisAlaCysAlaLeuAla 617  
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2964 AC 2965  
  
seq\_name: N\_Geneseq\_36:X02660  
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ID X02660 standard; DNA; 8192 BP.  
AC X02660;  
DT 07-MAY-1999 (first entry)  
DE EP-892047 Seq ID 36.  
KW Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;  
KW organ transplantation; inflammation therapy; immunotherapy; agonist;  
KW immunomodulatory; antagonist; ss.  
OS Homo sapiens.  
PN EP-892047-A2.  
PD 20-JAN-1999.  
PF 06-JUL-1998; 112470.  
PR 11-FEB-1998; DE-005371.



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seq\_name: N\_Geneseq\_36:X02661

seq\_documentation\_block:

ID X02661 standard; DNA; 7000 BP.

AC X02661;

DT 07-MAY-1999 (first entry)

DE EP-892047 Seq ID 37.

KW Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;

KW organ transplantation; inflammation therapy; immunotherapy; agonist;

KW immunomodulatory; antagonist; ss.

OS Homo sapiens.

PN EP-892047-A2.

PD 20-JAN-1999.

PF 06-JUL-1998; 112470.

PR 11-FEB-1998; DE-005371.

PR 09-JUL-1997; DE-029211.

PA (HMR1) HOECHST MARION ROUSSEL DEUT GMBH.

PI Ensser A, Fleckenstein B;

DR WPI; 99-083564/08.

PT New semaphorin L proteins - used as immunosuppressants and

PT antiinflammatory agents in organ transplants, inflammation therapy,

PT immunotherapy and gene therapy

PS Disclosure; Page 91-95; 135pp; German.

CC This invention describes a novel human semaphorin L protein. This protein

CC or its encoding DNA are useful as immunosuppressants and/or

CC anti-inflammatory agents in organ transplantation, inflammation therapy,

CC immunotherapy and gene therapy. The DNA can be used to produce knock-out

CC or knock-in animals for research purposes. The proteins or DNA can be

CC used to search for the corresponding receptors or to screen for

CC immunomodulatory agonists or antagonists.

SQ Sequence 7000 BP; 1586 A; 1940 C; 1050 G; 1624 T;

alignment\_scores:

Quality: 3443.00

Length: 634

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Ratio: 5.431 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-041-236-2 x X02661
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643 CTGCTGCTGCTGCTGGGGCGCGCGCTCCGCCAGGGCCACCTAAG 692
17 gSerGlyProArgIlePheAlaValTrpLysGlyHisValGlyGlnAspA 34
693 GAGCGGACCCCGCATCTTCGCGCTCTGGAAGGCCATGTAGGCGCAGACC 742
34 rgValAspPheGlyGlnThrGluProHisThrValLeuPheHisGluPro 50
743 GGTGTGACTTTGGCCAGACTGAGCCGCACACGGTGTCTTTCCACGAGCCA 792
51 GlySerSerSerValTrpValGlyGlyArgGlyLysValTyrLeuPheAs 67
793 GCGAGCTCTCTGTGTGGGTGGAGGACGTGGCAAGGTCTACCTCTTTGA 842
67 pPheProGluGlyLysAsnAlaSerValArgThrValAsnIleGlySert 84
843 CTTCGCCGAGGGCAAGAACGCATCTGTGCGCACGGTGAATATCGGCTCCA 892
84 hrlYsGlySerCysLeuAspLysArgAspCysGluAsnTyrIleThrLeu 100
893 CAAGGGGTCTCTGTGATAAGCGGGACTGCGAGAACTACATCACTCTC 942
101 LeuGluArgArgSerGluGlyLeuLeuAlaCysGlyThrAsnAlaArgHI 117
943 CTGGAGAGCGGAGTGAGGGGCTGTGGCTGTGGCCACCAACCCCGGCA 992
117 sProSerCysTrpAsnLeuValAsnGlyThrValValProLeuGlyGluM 134
993 CCCACGCTGCTGGAACCTGTGTAATGGCACTGTGGTGCCACTTGGCGAGA 1042
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1543 GCCGCTCTGTGTATTCCTCCGCTGACATTGACAAGGTCTTCCGTACTC 1592
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1593 CTCCTCAAGGCTACCACCTCAAGCCCTCCCAACCCCGCGCTGGCAAGT 1642
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2443 GACGGCATCATGCGCGAGCACCTGCTGGTCATGCTGCGCTGGCTGG 2492
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634 is 634
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2543 AC 2544

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seq\_name: N\_Geneseq\_36:X02662

seq\_documentation\_block:

ID X02662 standard; DNA; 7108 BP.

AC X02662:

DT 07-MAY-1999 (first entry)

DE EP-892047 Seq ID 38.

KW Semaphorin L; human; immunosuppressant; anti-inflammatory; agonist;

KW organ transplantation; inflammation therapy; immunotherapy; antagonist;

OS Homo sapiens.

PN EP-892047-A2.

PD 20-JAN-1999.

PF 06-JUL-1998; 112470.

PR 11-FEB-1998; DE-005371.

PR 09-JUL-1997; DE-029211.

PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.

PI Ensser A, Fleckenstein B;

DR WPI; 99-083564/08.

PT New semaphorin L proteins - used as immunosuppressants and

PT anti-inflammatory agents in organ transplants, inflammation therapy,

PT immunotherapy and gene therapy

PS Disclosure: Page 96-100; 135pp; German.

CC This invention describes a novel human semaphorin L protein. This protein

or its encoding DNA are useful as immunosuppressants and/or

CC anti-inflammatory agents in organ transplantation, inflammation therapy,

CC immunotherapy and gene therapy. The DNA can be used to produce knock-out

CC or knock-in animals for research purposes. The proteins or DNA can be

CC used to search for the corresponding receptors or to screen for

CC immunomodulatory agonists or antagonists.

SQ Sequence 7108 BP; 1617 A; 1970 C; 1875 G; 1646 T;

alignment\_scores:

Quality: 3443.00

Ratio: 5.431

Percent Similarity: 100.000

Percent Identity: 100.000

alignment\_block:

US-09-041-236-2 x X02662

Align s.g 1/1 to: X02662 from: 1 to: 7108

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634 Is 634  
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2543 AC 2544

seq\_name: N\_Geneseq\_36:X02627

## seq\_documentation\_block:

ID X02627 standard; DNA; 2636 BP.  
 AC X02627;  
 DT 07-MAY-1999 (first entry)  
 DE EP-892047 Seq ID 1.  
 KW Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;  
 KW organ transplantation; inflammation therapy; immunotherapy; agonist;  
 KW immunomodulatory; antagonist; ss.  
 OS Homo sapiens.  
 PN EP-892047-A2.  
 PD 20-JAN-1999.  
 PE 06-JUL-1998; 112470.  
 PR 11-FEB-1998; DE-005371.  
 PR 09-JUL-1997; DE-029211.  
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.  
 PI Ensser A, Fleckenstein B;  
 DR WPI; 99-083564/08.  
 PT New semaphorin L proteins - used as immunosuppressants and  
 PT antiinflammatory agents in organ transplants, inflammation therapy,  
 PT immunotherapy and gene therapy  
 PS Disclosure; Page 58-60; 135pp; German.  
 CC This invention describes a novel human semaphorin L protein. This protein  
 CC or its encoding DNA are useful as immunosuppressants and/or  
 CC anti-inflammatory agents in organ transplantation, inflammation therapy,  
 CC immunotherapy and gene therapy. The DNA can be used to produce knock-out  
 CC or knock-in animals for research purposes. The proteins or DNA can be  
 CC used to search for the corresponding receptors or to screen for  
 CC immunomodulatory agonists or antagonists.  
 SQ Sequence 2636 BP; 536 A; 835 C; 764 G; 501 T;

## alignment\_scores:

Quality: 3443.00 Length: 634  
 Ratio: 5.431 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-041-236-2 x X02627

Align seg 1/1 to: X02627 from: 1 to: 2636

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 17 gSerGlyProArgIlePheAlaValTriPlysGlyHisValGlyGlnAspA 34  
 159 GAGCGGACCCGCATCTTCGCCGCTGGAAGGCCATGTAGGGCAGGACC 208  
 34 rgValAspPheGlyClnThrGluProHisThrValLeuPheHisGluPro 50  
 209 GGGTGGACTTTGGCCAGACTGAGCGGCACAGCGTGTCTTTCACAGCCA 258  
 51 GlySerSerValTriPValGlyArgGlyLysValTyrLeuPheAs 67  
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 309 CTTCCCGAGGCAAGACGCATCTGCGCACGGTGATATCGGCTCCA 358  
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 459 CCCAGCTGCTGGAACTGTGTGAATGGCACTGTGTGCTCACTTGGCGAGA 508

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 217 oAspLysAsnProGluAlaProLeuAsnValSerArgValAlaGlnLeu 234  
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 351 ArgHisProGluValAlaGlnArgValGluProMetGlyProLeuLysTh 367  
 1159 GGTCAACCCAGAGGTGGCGAGGGTGGAGCCCATGGGGCTCTGAAGAC 1208  
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1409 AGACCATGTCGCTGGATGCTGAGCGGAGAGTGTATGTGAGTCCAG 1458
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601 AspGlyIleMetAlaGluHisLeuLeuGlyHisAlaCysAlaLeuAla 617
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seq\_name: N\_Geneseq\_36:X02658

seq\_documentation\_block:

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ID X02658 standard; DNA; 5856 BP.
AC X02658;
DT 07-MAY-1999 (first entry)
DE EP-892047 Seq ID 34.
KW Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;
KW organ transplantation; inflammation therapy; immunotherapy; agonist;
KW immunomodulatory; antagonist; ss.
KW Homo sapiens.
PN EP-892047-A2.
PD 20-JAN-1999.
PF 06-JUL-1998; 112470.
PR 11-FEB-1998; DE-005371.
PR 09-JUL-1997; DE-029211.
PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
PI Ensser A, Fleckenstein B;
DR WPI: 99-083564/08.
PT New semaphorin L proteins - used as immunosuppressants and
PT antinflammatory agents in organ transplants, inflammation therapy,
immunotherapy and gene therapy

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PS Example 7; Page 77-80; 135pp; German.  
 CC This invention describes a novel human semaphorin L protein. This protein  
 CC or its encoding DNA are useful as immunosuppressants and/or  
 CC anti-inflammatory agents in organ transplantation, inflammation therapy,  
 CC immunotherapy and gene therapy. The DNA can be used to produce knock-out  
 CC or knock-in animals for research purposes. The proteins or DNA can be  
 CC used to search for the corresponding receptors. The proteins or DNA can be  
 CC immunomodulatory agonists or antagonists.  
 SQ Sequence 5856 BP; 1262 A; 1575 C; 1699 G; 1320 T;

alignment\_scores:

Quality: 3443.00 Length: 634  
 Ratio: 5.431 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-041-236-2 x X02658/rev ..

Align seg 1/1 to reverse of: X02658 from: 1 to: 5856

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17 gSerGlyProArgIlePheAlaValTrpLysGlyHisValGlnAspA 34
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2094 GAGCGACCCCGCATCTTCGCCGCTCTGGAAGGCCATGTAGGCGAGACC 2045
34 rgValAspPheGlyGlnThrGluProHisThrValLeuPheHisGluPro 50
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2044 GGGTGGACTTTGGCCAGACTGAGCCGACACGCGTCTTTTCCACGAGCCA 1995
51 GlySerSerSerValTrpValGlyGlyArgGlyLysValTyrLeuPheAs 67
1994 GCGAGCTCTCTGCTGGGTGGGAGGACGTGGCAAGGTCTACTCTTTGA 1945
67 pPheProGluGlyLysAsnAlaSerValArgThrValAsnIleGlySerT 84
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84 hrLysGlySerCysLeuAspLysArgAspCysGluAsnTyrIleThrLeu 100
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217 oASpLysAsnProGluAlaProLeuAsnValSerArgValAlaGlnLeuC 234  
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 517 aProLeuGlnLysValSerLeuAlaProAsnSerArgTyrrTyrrLeuSerC 534

534 CCCACTGCAGAAGGTTTCCCTGGCCCCAAACTCTCGTACTACTGAGCT 545  
 534 ySPrometGluSerArgHisAlaThrTyrrSerTrpArgHisLysGluAsn 550  
 544 GCCCATGGAATCCCGCACGCCACCTACTCATGCGGCCCAAGAGAAC 495  
 551 ValGluGlnSerCysGluProGlyHisGlnSerProAsnCysIleLeuPh 567  
 494 GTGAGCAGAGCTCGAACCCTGGTCACGAGAGCCCAACTGCATCTCTGT 445  
 567 eIleGluAsnLeuThrAlaGlnGlnTyrrGlyHisTyrrPheCysGluAlaG 584  
 444 CATCGAAGACCTCACGGCGCAGCAGTAGTACGGCCACTACTTTCGCGAGGCC 395  
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 244 AC 243

seq\_name: N\_Geneseq\_36:X02666

seq\_documentation\_block:

ID X02666 standard; DNA; 6622 BP.

AC X02666;

DT 07-MAY-1999 (first entry)

DE EP-892047 Seq ID 42.

KW Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;

KW organ transplantation; inflammation therapy; immunotherapy; agonist;

KW immunomodulatory; antagonist; ss.

OS Homo sapiens.

PN EP-892047-A2.

PD 20-JAN-1999.

PF 06-JUL-1998; 112470.

PR 11-FEB-1998; DE-005371.

PR 09-JUL-1997; DE-029211.

PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Esser A, Fleckenstein B;

DR WPI; 99-083564/08.

PT New semaphorin L proteins - used as immunosuppressants and

PT art inflammatory agents in organ transplants, inflammation therapy,

PT immunotherapy and gene therapy

PS Disclosure: Page 112-116; 135pp; German.

CC This invention describes a novel human semaphorin L protein. This protein

CC or its encoding DNA are useful as immunosuppressants and/or

CC anti-inflammatory agents in organ transplantation, inflammation therapy,

CC immunotherapy and gene therapy. The DNA can be used to produce knock-out

CC or knock-in animals for research purposes. The proteins or DNA can be

CC used to search for the corresponding receptors or to screen for

CC immunomodulatory agonists or antagonists.

SQ Sequence 6622 BP; 1584 A; 1720 C; 1701 G; 1617 T;

alignment\_scores:

Quality: 3308.00

Ratio: 5.450

Percent Similarity: 100.000

Percent Identity: 100.000

alignment\_block:

US-09-041-235-2 x X02666

align seg 1/1 to: X02666 from: 1 to: 6622

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27 sGlyHisValGlyGlnAspArgValaspPheGlyGlnThrGluProHist 44  
221 AGCCCATGTAGGCGAGGACCGGGTGGACTTTGGCCAGACTGAGCCGACA 270  
44 hrValLeuPheHisGluProGlySerSerValTrpValGlyGlyArg 60  
271 CGGTGCTTTTCCACGAGCAGGAGCGTCTCTGTGGGTGGAGGACGT 320  
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77 gThrValAsnIleGlySerThrLysGlySerCysLeuAspLysArgAspC 94  
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127 rValValProLeuGlyGluMetArgGlyTyrAlaProPheSerProAspG 144  
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611 HisAlaCysAlaLeuAlaAla 617





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284 TrpArgAspThrArgValTyrGlyValPheSerAsnProTrp..... 297
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3901 TGGGTCTTGGGCCCCCATTTAGCTGGTCTCCATGTCACTGCAGGAACCT 3950  
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316 hrSerSerLeuLysGlyTyrHisSerSerLeuProAsnProArgProGly 332  
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6701 CAGGCTGCCCTTAGGCTCCACATCTTCCACAGTCAGGCTCTCTCTGCC 6750  
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6851 CTGACCTCTGTCCACCATACACAGACAGGGGCACATATCCCAAGGTGGT 6900  
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6901 GGAACGGGGGAGCAGGAGCACAGCTTCGCCTTCAACATCATGGAGATCC 6950  
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7001 CGGCTGAGCCTTCCCCCACTCGCTGCCATGGGCTATGCAGTGACTGCAGC 7050  
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7501 CTGCTGATCTCTTCTCTCTCTCCATCCAGTCCAGGTCACTGTGCAATCCAT 7550  
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7951 TACCTGAGCTGCCCATGGAATCCCGCCACGCCACCTACTCATGGCGCCA 8000  
547 sLysGluAsnValGluGlnSerCysGluProGlyHisGlnSerProAsnC 564  
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8151 GCTGCCCGGAGGAGCGCATCATGGCCGAGCAGCTGCTGGGTGATGCTGTG 8200  
614 lAlaLeuAlaAlaSerLeuTrpLeuGlyValLeuProThrLeuThrLeuGly 630  
8201 CCTTGGCGGCTCTCTCTGCTGGGGGTGCTGCCACACTCACTCTTTGGC 8250  
631 LeuLeuValHis 634  
8251 TTGCTGTGTCAC 8262

seq\_name: N\_Geneseq\_36::X02628

seq\_documentation\_block:

ID X02628 standard; DNA; 1195 BP.

AC X02628:

DT 07-MAY-1999 (first entry)

DE EP-992047 Seq ID 2.

KW Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;  
organ transplantation; inflammation therapy; immunotherapy; agonist;

OS Immunomodulatory; antagonist; ss.

PN Homo sapiens.

PR 992047-A2.

PC 20-JAN-1999.

PF 05-JUL-1998; 112470.

PR 11-FEB-1998; DE-005371.

PR 09-JUL-1997; DE-029211.

PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Ensser A, Fleckenstein B;

DK WPI; 99-083564/08.

PT New semaphorin L proteins - used as immunosuppressants and

700 CAAGACCAAGCCTATGATGATATAGATCTACTACTTCTCCGAGAAGACA 749

216 nProAspLysAsnProGluAlaProLeuAsnValSerArgValAlaGlnL 233

750 CCTGTACAGAACCCCGAGGCTCTCTCAATGTGTCCGAGTAGCCCACT 799

233 euCysArgGlyAspGlnGlyGlyLysSerSerLeuSerValSerLysTrp 249

800 TGTGTGACGGGGGACACAGGTTGTGTGAGAGTTCTGTGTCTGTCTCCAACTGG 849

250 AsnThrPheLeuLysAlaMetLeuValCysSerAspAlaAlaThrAsnLys 266

266 sasNpHeAsnArgLeuGlnAspValPheLeuLeuProAspProserGlyG 283  
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850 AACACCTTCTCTGAAGGCCATGTTGGTCTCTGACGATGTCAGCACCACACAG 895

283 lnTrpArgAspThrArgValTyrGlyValPheSerAsnProTrpAsnTyr 299

350 AATGGAGAGATACCAAGGCTCTATGGCTTTCTCCACCCCCCTGGGACTAC 355

Accession	Gene	Protein	Length
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316	rSerSerLeuLysGlyTyrHisSerSerLeuProAsnProArgProGlyL	rSerSerLeuLysGlyTyrHisSerSerLeuProAsnProArgProGlyL	333
1050	CTCATCGCTCAAGAGCTACACATGGCGCTTCCAAACCTCGACCTGGCA	CTCATCGCTCAAGAGCTACACATGGCGCTTCCAAACCTCGACCTGGCA	1099
333	ysCysLeuProAspGlnGlnProIleProThrGluThrPheGlnValala	ysCysLeuProAspGlnGlnProIleProThrGluThrPheGlnValala	349
1100	TGTGCGCTCCCAAAAAAGCAGCCCATACCCACAGAAACCTTCCAGGTAGCT	TGTGCGCTCCCAAAAAAGCAGCCCATACCCACAGAAACCTTCCAGGTAGCT	1149
350	AspArgHisProGluValalaGlnArgValGluProMetGlyPro	AspArgHisProGluValalaGlnArgValGluProMetGlyPro	364
1150	GATGATCACCCAGAGGTGGCTCAGAGGGTGGAACTATGGGGCCC	GATGATCACCCAGAGGTGGCTCAGAGGGTGGAACTATGGGGCCC	1194
Name: N_Geneseq_36:X02663			
Documentation_block:			
X02663 standard; DNA; 4019 BP.			
X02663;			
07-MAY-1999 (first entry)			
EP-892047 Seq ID 39.			
Semaphorin L; human; immunosuppressant; anti-inflammatory;			
organ transplantation; inflammation therapy; immunotherapy;			
immunomodulatory; antagonist; ss.			
Homo sapiens.			
EP-892047-A2.			
20-JAN-1999.			
06-JUL-1998; 112470.			
11-FEB-1998; DE-005371.			
09-JUL-1997; DE-029211.			
(HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.			
Enser A, Fleckenstein B;			
WPI; 99-0833564/08.			
New semaphorin L proteins - used as immunosuppressants and			
antiinflammatory agents in organ transplants, inflammation			
immunotherapy and gene therapy.			
Disclosure; page 100-103; 135pp; German.			
This invention describes a novel human semaphorin L protein			
or its encoding DNA are useful as immunosuppressants and/or			
anti-inflammatory agents in organ transplantation, inflamma			
immunotherapy and gene therapy. The DNA can be used to prod			
or knock-in animals for research purposes. The proteins or			
used to search for the corresponding receptors or to screen			
immunomodulatory agonists or antagonists.			
Sequence 4019 BP; 1033 A; 996 C; 975 G; 1015			
ment_scores:			
Quality: 1069.00			
Length: 200			

Length: 200

Ratio: 5.345 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 99.500  
alignment\_block:  
US-09-041-236-2 x X02663  
Align seg 1/1 to: X02663 from: 1 to: 4019

146 SerLeuValLeuPheGluGlyAspGluValTyrSerThrIleArgLysG1 162  
148 TCCCTGGTTCCTGTTGAAGGGACGAGGTGATTCCACCATCCGGAAGCA 197  
162 nGluTyrAsnGlyLysIleProArgPheArgIleArgGlyGluSerG 179  
198 GGAATACAAATGGGAAGATCCCTCGGTTCGCGCATCCGGCGGAGAGTG 247  
179 LuLeuTyrThrSerAspThrValMetGlnAsnProGlnPheIleLysAla 195  
248 AGCTGTACACCACTGATCTGTCATGCAGAACCCACAGTTTATCAAGCC 297  
196 ThrIleValHisGlnAspGlnAlaTyrAspLysIleTyrTyrPhePh 212  
298 ACCATCGTGCACCAAGACGAGCTTACGATGACAAGATCTACTACTTCT 347  
212 eArgGluAspAsnProAspLysAsnProGluAlaProLeuAsnValSerA 229  
348 CCGAGAGACAAATCTGACAAAGATCTCTGAGGCTCTCTCAATGTGTCC 397  
229 rGValAlaGlnLeuCysArgGlyAspGlnGlyGlyGluSerSerLeuSer 245  
398 GTGTGGCCAGTTGTGAGGGGGACCGAGGTGGGGAAGTTCACTGTCA 447  
246 ValSerLysTyrAsnThrPheLeuLysAlaMetLeuValCysSerAspAl 262  
448 GTCTCAAGTGGACACATTTCTGAAAGCCATGCTGTGTATGCAGTGATGC 497  
262 aAlaThrAsnLysAsnPheAsnArgLeuGlnAspValPheLeuProA 279  
498 TGCCACCAACAAAGAACTTCAACAGGCTGCAAGACGCTCTCTGCTCCCTG 547  
279 sProSerGlyGlnTrpArgAspThrArgValTyrGlyValPheSerAsn 295  
548 ACCCGAGCGGCGAGTGGAGGACACAGGGTCTATGGTGTTCCTCCAAC 597  
296 ProTrpAsnTyrSerAlaValCysValTyrSerLeuGlyAspIleAspLy 312  
598 CCTTGGAACTACTACGCGTGTGTGTATTCCTCGGTGACATTGACAA 647  
312 sValPheArgThrSerSerLeuLysGlyTyrHisSerSerLeuProAsn 329  
648 GGTCTTCGGTACCTCCTCACTCAAGGGCTACCACTCAAGGCTTCCCAACC 697  
329 roArgProGlyLysCysLeuProAspGlnGlnProIleProThrGluThr 345  
698 CGCGCCCTGGGAAGTGCCTCCAGACGACGACCGCATACCCACAGAAAGC 747

seq\_name: N\_Geneseq\_36:X02664

seq\_documentation\_block:  
ID X02664 standard; DNA; 3999 BP.  
AC X02664;  
DT 07-MAY-1999 (first entry)  
DE EP-892047 Seq ID 40.  
KW Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;  
KW organ transplantation; inflammation therapy; immunotherapy; agonist;  
KW immunomodulatory; antagonist; ss.  
OS Homo sapiens.  
PN EP-892047-A2.  
PD 20-JAN-1999.  
PF 06-JUL-1998; 112470.  
PR 11-FEB-1998; DE-005371.  
PR 09-JUL-1997; DE-029211.  
PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.

PI Ensser A, Fleckenstein B;  
DR WPI; 99-083564/08.  
PT New semaphorin L proteins - used as immunosuppressants and  
PT anti-inflammatory agents in organ transplants, inflammation therapy,  
PT immunotherapy and gene therapy  
PS Disclosure; Page 103-105; 135pp; German.  
CC This invention describes a novel human semaphorin L protein. This protein  
CC or its encoding DNA are useful as immunosuppressants and/or  
CC anti-inflammatory agents in organ transplantation, inflammation therapy,  
CC immunotherapy and gene therapy. The DNA can be used to produce knock-out  
CC or knock-in animals for research purposes. The proteins or DNA can be  
CC used to search for the corresponding receptors or to screen for  
CC immunomodulatory agonists or antagonists.  
SQ Sequence 3999 BP: 1001 A; 1021 C; 986 G; 991 T;

alignment\_scores:  
Quality: 1049.00 Length: 189  
Ratio: 5.550 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.942  
alignment\_block:  
US-09-041-236-2 x X02664  
Align seg 1/1 to: X02664 from: 1 to: 3999

446 TyrValSerSerGlnTrpGluValSerGlnValProLeuAspLeuCysG1 462  
154 CATGGAGCTCCAGTGGAGGTGAGCCAGGTGCCCTGGACCTGTGTGA 203  
462 uValTyrGlyGlyCysHisGlyCysLeuMetSerArgAspProTyrC 479  
204 GGTCTATGGCGGGCTGCCACGTTGCTCTCATGTCCGAGACCCCTACT 253  
479 ysGlyTrpAspGlnGlyArgCysIleSerIleTyrSerSerGluArgSer 495  
254 CGCGCTGGGACGAGGGCGGTGCATCTCCATCTACAGCTCCGAAAGCTCA 303  
496 ValLeuGlnSerIleAsnProAlaGluProHisLysGluCysProAsnPr 512  
304 GTGCTGCATTCATTAATCCAGCGGACGACCAAGAGGTGTCCCAACC 353  
512 oLysProAspLysAlaProLeuGlnLysValSerLeuAlaProAsnSerA 529  
354 CAACACGACAAAGCCCACTGCAGAGGTTTCCCTGGCCCAAACTCTC 403  
529 rGTYrTyrLeuSerCysProMetGluSerArgHisAlaThrTyrSerTrp 545  
404 GCTACTACCTGAGCTGCCCATGGAATCCCGCCACGACCTACTCATFG 453  
546 ArgHisLysGluAsnValGluGlnSerCysGluProGlyHisGlnSerPr 562  
454 CGCCACAGAGAGACGTTGAGCAGACGCTGCCAAGCTGTGTACACGAGCC 503  
562 oAsnCysIleLeuPheIleGluAsnLeuThrAlaGlnGlnTyrGlyHisT 579  
504 CAACTGCATCTCTTTCATCGAGAACTTCACGCGCAGCAGTACGGCCACT 553  
579 yrPheCysGluAlaGlnGluGlySerTyrPheArgGluAlaGlnHisTrp 595  
554 ACTTCTCGAGGCGCCAGGAGGGCTCTACTTCCGCGAGGCTCAGCAGCTGG 603  
596 GlnLeuLeuProGluAspGlyIleMetAlaGluHisLeuLeuGlyHisAl 612  
604 CAGTGTGCTGCCGAGGAGCGGATCATGGCCGAGCACCTGTCTGGGTGATGC 653  
612 aCysAlaLeuAlaAlaSerLeuTrpLeuGlyValLeuProThrLeuThrL 629  
654 CTGTGCGCTGTGCTGCCCTCCCTCTGTGCTGGGGGTGCTGCCACACTCACTC 703  
629 euGlyLeuLeuValHis 634  
704 TTGCTTGTGTGTCAC 720

seq\_name: N\_Geneseq\_36:Q87442

seq\_documentation\_block:  
ID Q87442 standard; CDNA; 2601 BP.

AC Q87442;

DT 21-NOV-1995 (first entry)

DE Human semaphorin III cDNA.

KW Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium;

KW varicella major virus; smallpox; semaphorin receptor binding activity;

KW modulation; nerve cell growth; immune response; viral pathogenesis;

KW neurological disease; neuro-regeneration; oncological infection; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT 16..2331

FT /\*tag= a

FT /product= human semaphorin III

FT W09507706-A.

PN 23-MAR-1995.

PD 13-SEP-1994; U10151.

PR 13-SEP-1993; US-121713.

PA (REGC ) UNIV CALIFORNIA.

PI Bentley DR, Goodman CS, Kolodkin AL, Matthes D;

PI O'Connor T;

DR WPI; 95-131177/17.

DR P-PSDB; R71380.

PT New class of semaphorin peptide(s) and polypeptide(s) - are

PT potent modulators of nerve cell growth and regeneration

PS Example 2; Page 60-63; 101pp; English.

CC The sequence of the cDNA encoding the human semaphorin III protein.

CC The proteins encoded by the grasshopper semaphorin I (Q87441), human

CC semaphorin III, vaccinia virus semaphorin IV (Q87443), Drosophila

CC semaphorin I and II (Q87444-45), Tribolium semaphorin I (Q87446) or

CC varicella major (smallpox) virus semaphorin IV (Q87447) genes were used to

CC generate a series of peptides (R70370-R70418), which retain semaphorin

CC receptor binding activity. The semaphorin derived or semaphorin receptor

CC derived peptides are potent modulators of nerve cell growth, immune

CC responsiveness and viral pathogenesis. They can be used in diagnosis and

CC treatment of neurological disease and neuro-regeneration, immune

CC modulation and diagnosis and treatment of viral and oncological infection

CC and diseases.

SQ Sequence 2601 BP; 809 A; 533 C; 593 G; 666 T;

alignment\_scores:

Quality: 649.50

Ratio: 1.620

Percent Similarity: 58.370

Length: 687

Gaps: 27

Percent Identity: 28.093

alignment\_block:

US-09-041-236-2 x Q87442 ..

Align seg 1/1 to: Q87442 from: 1 to: 2601

1 LeuLeuLeuLeuLeuTrpAlaAlaAlaSerAlaGlnGlyHisLeuAr 17

17 gSerGly.....ProArgIlePheAlaValTrpLysGlyHisV 30

84 GAATGGGAAGAACAATGTGCCAAGGCTGAATTTATCTACAAAGAAATGT 133

30 alGlyGlnAspArgValAsp.....PheGlyGlnThrGlu 41

134 TGAATCCCAACAATGTATGATCACTTTCAATGGCTGGCCACACAGCTCCAGT 183

42 ProHisThrValLeuPheHisGluProGlySerSerValTrpValG 58

184 TATCATACCTTCCTTTTGGATGAGGAA...CGGAGTAGGCTGTATGTTG 230

58 yGlyArgGlyLysValTrpLysPheAspPheProGluGlyLysAsnAla 75

231 AGCAAGGATCATATATTTTCATTCGACCTGTTTAAATCAAGGATTTTC 280

75 erValArgThrValAsnIleGlySerThrLys..... 85  
 281 AAAGATTGTGGCCAGTATCTTACACCAGAGAGATGAATCAAGTGG 330  
 86 ...GlySerCysLeuAspLysArgAspCysGluAsnTyrIleThrLeuLe 101  
 331 GCTGGAAGAGACATCTCTGAAA...GAATGTCTAATTTTCATCAAGTACT 377  
 101 uGluArgArgSerGlu...GlyLeuLeuAlaCysGlyThrAsnAlaArgH 117  
 378 TAAGCATATATACAGACTCTTGTACGCTGTGGACGGGGCTTTTC 427  
 117 isProSerCysTrpAsnLeuValAsnGlyThrValValProLeuGlyGlu 133  
 428 ATCCAAATTGC.....ACCTACATTGAATTTGGACAT 459  
 134 Met..... 134  
 460 CATCTGTAGGACAATATTTTAAAGCTGGAGAACTCACATTTTGAACCG 509  
 135 ArgGlyTyrAlaProPheSerProAspCysGluAsnSerLeuValLeuPheG 151  
 510 CCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAA 559  
 151 LuGlyAspGluValTyrSerThrIleArgLysGlnGluTyrAsnGlyLys 167  
 560 TAGATGGAGAATATATCTCTGGAACCTGCAGCTGATTTTATGGGGCCAGAC 609  
 168 IleProArgPheArgIleArgGlyGluSerGluLeuTyrThr..... 182  
 610 TTTGTATCTCTCGAACTCTTGGGACCACCACTCAATCAGGACAGACGA 659  
 183 ....SerAspThrValMetGlnAsnProGlnPheIleLysAlaThrIleV 198  
 660 GCATGCTCCAGGTGGCTCAATGATCCAAAGTTCATTTAGTCCCACTCA 709  
 198 aHisGln...AspGlnAlaTyrAspAspLysIleTyrTyrPhePheArg 213  
 710 TCTCAGAGAGTCACTCTCTGAAGATGACAAAGATATATCTTTTCTCCGT 759  
 214 GluAspAsnProAspLysAsnProGluAlaProLeuAsnValSerArgVa 230  
 760 GAAATGCAATAGATGGAGACACACTCTGGAAAAGCTACTCAGCTAGAA 809  
 230 lAlaGlnLeuCysArgGlyAspGlnGlyGlyGluSerSerLeuSerValS 247  
 810 AGGTGAGATATGCAAGATGACTTTGGAGGGCAGACAGAGTCTG...GTGA 856  
 247 erLysTrpAsnThrPheLeuLysAlaMetLeuValCysSerAspAlaAla 263  
 857 ATAATGGACACATCTCTCAAGAGCTCTGCTCTGATTTGCTCAGTCCAGGT 906  
 264 ThrAsn.....LysAsnPheAsnArgLeuGlnAspValPheLeuLe 277  
 907 CCAATGGCATTGACACTCTTTTGTATGAACTGCAGGATGTATCTCTAAT 956  
 277 u.....ProAspProSerGlyGlnTrpArgAspThrArgValTyrGlyV 292  
 957 GAACCTTAAAGATCTCT.....AAAACTCAGTTGTATATGGAG 994  
 292 aPhe.....SerAsnProTrpAsnTyrSerAlaValCysValTyr 305  
 995 TGTTCAGCACTTCCAGTACATTTTCAAGGGATCAGCGGTGTATGTAT 1044  
 306 SerLeuGlyAspIleAspLysValPhe..... 314  
 1045 AGCATGAGTGTGTGAGAAGGTGTTCTTGTCTCATATGCCACAGGGA 1094  
 315 ....ArgThrSerSerLeuLysGlyTyrHisSerSerLeuProAsnProA 330  
 1095 TGGACCCCACTATCAATGGGTGGCTTATCAAGGAAGAGTCCCTATCCAC 1144

```
330 rgProGlyLysCys.....LeuProAspGlnGln 339
||||| |||
1145 GCCCAGGAACCTGTCGCCAGCAAAACATTGGTGTGACTACAAAG 1194
||||| |||
340 ProfileProThrGluThrPheGlnValAlaAspArgHisProGluValAl 356
||||| |||
1195 GACCTCTCTGATGATGATATACCTTTGCAGAAAGTCATCCAGCCATGTA 1244
||||| |||
356 aGlnArgValGluProMetGly.....ProLeuLysThrProL 369
||||| |||
1245 CAATCCAGTGTTCCTATGAACAATCGCCCAATAGTATCAAAACGGAT 1294
||||| |||
369 euPheHisSerLysTyHisTyHisGlnLysValAlaValHisArgMetGln 385
||||| |||
1295 TA.....AATTATCAATTTACAAATTTGCGTAGACCGATGGAT 1335
||||| |||
386 AlaSerHisGlyGluThrPheHisValLeuTyLeuThrThrAspArgG1 402
||||| |||
1336 GCAGAAGATGCACAG...TATGATGTTATGTTTATCGGAACAGATGTGG 1382
||||| |||
402 yThrIleHisLysValValGlu...ProGlyGluGlnGluHisSerPhea 418
||||| |||
1383 GACCGTCTCTTAAGTAGTCTTCAATTCCTAAGGAGACTTGGTATGATTAG 1432
||||| |||
418 laPheAsnIleMet...GluIleGlnProPheArgArgAlaAlaIle 433
||||| |||
1433 AAGAGGTCTCTCTGGAAGAAATACAGTGTTCGGAACCGACTGCTATT 1482
||||| |||
434 GlnThrMetSerLeuAspAlaGluArgLysLeuTyValSerSerG1 450
||||| |||
1483 TCACCAATGGAGCTTCCACTAAGCAGCAACAATATATATGTTCTAAC 1532
||||| |||
450 nTrpGluValSerGlnValProLeuAspLeuCysGluValTyRgLyG 467
||||| |||
1533 GCGTGGGTGTCGCCAGCTCCCTTTACACCGGTGTGATATTACGGAAAG 1582
||||| |||
467 lyCysHisGlyCysLeuMetSerArgAspProTyRgCysGlyTrpAspGln 483
||||| |||
1583 CGTGTGTGAGTGTGCTGCCGAGACCCCTTACTGTCTGGATGGT 1632
||||| |||
484 GlyArgCysIleSerIleTyR.....SerSerGluArgSerValLeuG1 498
||||| |||
1633 TCTCATGTTCTCCCTATTTCCACTGCAAGAGAGCCACAGCAGCA 1682
||||| |||
498 nSerIleAsnProAlaGluProHisLysGluCysProAsnProLysProA 515
||||| |||
1683 AGATATAAGAAATGGAGACCCACTGACTCTACTGTTACAGCTTACACCAT 1732
||||| |||
515 spLys.....AlaProLeuGlnLysValSerLeu...AlaPro 526
||||| |||
1733 ATAATCACCATGGCCACAGCCCTGAAGAGAGAAATCATCTATGGGTAGAG 1782
||||| |||
527 AsnSerArgTyTyRLeuSerCysProMetGluSerArgHisAlaThrTy 543
||||| |||
1783 AATAGTAGCACATTTTGGATGAGTCAGTCCGAAGTCGCAGAGCGCTGGT 1832
||||| |||
543 rSerTrpArgHisLysGluAsnValGluGlnSerCysGluProGlyHisG 560
||||| |||
1833 CTATTGGCAATTCAGAGCGGCAATTAAGAGAGCGAAAGAGAGATCAGAG 1882
||||| |||
560 lnSerProAsnCysIle.....LeuPheIleGluAsnLeu 571
||||| |||
1883 TGGATGATCATPATCATCAGGACAGATCAAGCCCTCTGCTACGATGCTA 1932
||||| |||
572 ThrAlaGlnGlnTyRgLyHisTyPheCysGluAlaGlnGluGlySerTy 588
||||| |||
1933 CAACAGAGAGGATTCAGGCAATTAATCTCTGCGGTGGGAAACATGGGT 1982
||||| |||
588 rPheArgGluAlaGlnHisTrpGlnLeuLeuProGluAspGlyIleMetA 605
||||| |||
1983 CATACAAACTCTCTTAAGGTAAACCTG.....GAAGTCATTGACA 2023
||||| |||
605 laGluHisLeu 608
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```
seq_name: N_Geneseq_36:T60666
seq_documentation_block:
ID T60666 standard; CDNA: 4391 BP.
AC T60666;
DT 24-JUL-1997 (first entry)
DE Mouse CD100 antigen cDNA.
KW CD100 antigen; semaphorin; leukocyte; B cell; T cell; lymphocyte;
KW vaccine; ss.
OS Mus sp.
FH Key
FT cds Location/Qualifiers
   434..3019
   /*tag= a
FT signal_peptide 434..556
   /*tag= b
FT mat_peptide 557..3016
   /*tag= c
PN W09717368-Al.
PD 15-MAY-1997.
PE 12-NOV-1996; U18645.
PR 09-NOV-1995; US-556422.
PA (DAND ) DANA FARBER CANCER INST.
PI Bousiotis V, Freeman GU, Hail KT, Nadler LM, Schultze JL;
DR P-PSDB; W17658.
PT Nucleic acid molecule encoding CD100 antigen - which stimulates
PI leukocyte response, e.g. B cell aggregation, differentiation,
PI survival and T cell proliferation
PS example 8; Page 81-85; 135pp; English.
CC A cDNA molecule (T60666) codes for mouse CD100 antigen (W17658) a
CC novel leukocyte semaphorin-like protein that stimulates a leukocyte
CC response, including B cell aggregation, B cell differentiation, B
CC cell survival and/or T cell proliferation. It was isolated from a
CC a cDNA library prep. from murine t cells activated with anti-CD3
CC and anti-CD28 antibodies using a probe corresponding to the
CC semaphorin and Ig domains of the human CD100 sequence (see also
CC T60666). CD100 nucleic acids, antisense sequences, recombinant
CC vectors, host cells expressing CD100, and CD100 polypeptides can
CC be utilised in diagnostic and therapeutic methods involving
CC modulation of B and T cell responses, neuron axonal growth and
CC immune cell-nerve cell interaction.
SQ Sequence 4391 BP; 1009 A; 1180 C; 1105 G; 1097 T;
```

## alignment\_scores:

Quality: 594.00 Length: 695  
Ratio: 1.543 Gaps: 32  
Percent Similarity: 55.396 Percent Identity: 28.201

## alignment\_block:

US-09-041-236-2 x T60666 ..

Align seq 1/1 to: T60666 from: 1 to: 4391

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1 LeuLeuLeuLeuLeuTyRAlaAlaAlaAlaSerAlaGlnGlyHisLeuAr 17
||||| |||
473 CTGGTGTGATGTTGAGAACCGCGGTGGCATTGCA..... 508
||||| |||
17 gSerGlyProArgIlePheAlaValTrpLys...GlyHisValGlyGlnA 33
||||| |||
509 .CCGTGTCCTCGGCTC.....ACCTGGGAACATGGAGAGTAGGT.... 547
||||| |||
33 spArgValAspPheGlyGlnThrGluProHisThrValLeuPheHisGlu 49
||||| |||
548 .....CTGGTGCAGTTTCACAAG 565
||||| |||
50 ProGly.....SerSerSe 54
||||| |||
566 CCAGGCATCTTTAACTACTGCGCCTTCTGATGAGTGAGGACAAAGACAC 615
```







```

346 PheGlnValAlaAspArgHisProGluValAlaGlnArgValGluProMe 362
      :|||:||||| :|||: :|||: :|||: :|||: :|||:
1436 GTCACCTTTTATTCGGAACCATCTCTCATGTACAATTCATCTACCCAAAT 1485
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
362 tGlyProLeuLysThrProLeu.....PheHisSerLysTyrHisT 376
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1486 CCAC.....AAAGGCTTTGATGTTCTCGTATTCGCACTGACTACAAGT 1529
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
376 yGlnLysValAlaValHisArgMetGlnAlaSerHisGlyGluThrPhe 392
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1530 ACACAAAGATAGCTGTGGATCGAGTGAAGCTGCTGATGGGAGA...TAC 1576
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
393 HisValLeuTyrLeuThrThrAspArgGlyThrIleHisLysValValG 409
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1577 CATGCTCTGTTCTCGCAACAGATCGGGTACTGTGCAAAAAGTGTGT 1626
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
409 u...ProGlyGluGlnGluHisSerPheAlaPheAsnIleMetGluIleG 425
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1627 TCTCTCTACTAACACTCTGTCTAGTGGCGAGCTCATCTTGGGAGGAGCTGG 1676
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
425 lnProPheArgArgAlaAlaAlaIleGlnThrMetSerLeuAspAlaGlu 441
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1677 AGCTCTTTAAGATCATGCTCTCTATACACATGAAATTTTCATCTAAA 1726
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
442 ArgArgLysLeuTyrValSerSerGlnTrpGluValSerGlnValProLe 458
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1727 AGCAACAGTTGATGTAGTTCCATGAAGGGTTTCCAGGTATCTCT 1776
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
458 uaspLeuGluValTyrGlyGlyCysHisGlyCysLeuMetSerA 475
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1777 GCACCCCTGCCACATCATGTGTACAGCTGTGCTGCTGCTGCCGCGC 1826
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
475 iqAspProTyrCysGlyTyrAspGlnGlyArgCysIleSerIleTyr... 490
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1827 GGGACCTTATTCGGCTGGGATGGCCATCTCTGTTCCAGATTCACCCA 1876
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
491 ...SerSerGluArgSerValLeuGlnSerIleAsnProAlaGluProH 506
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1877 ACTGGGAAACGGAGGAGCGAAGACAAAGATGTGAGACATGGAAACCCACT 1926
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
506 slyGluCysPro.....AsnProLysProAspLysAlaProLeuGlnL 521
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1927 GACTCAATCGACAGGATTAATCTTAAAGACATACAGAAATGCGAGTGA 1976
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
521 ysValSerLeu...AlaProAsnSerArgTyrTyrLeuSerCysProMet 536
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1977 TTGTGAGTATGGAGTAAATAATAACACCACTTTCTGGAGTGTGCCCCC 2026
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
537 GluSerArgHisAlaThrTyrSerTrp.....Ar 546
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
2027 AAGTCTCCGACGACATCTATCAAGTGGCTGTACAGAAAGACAAAGACAG 2076
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
546 gHisLysGlu...AsnValGluGlnSerCysGluProGlyHisGlnSerP 562
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
2077 GAGGAAAGAGGTTAAGTGAATGAACGAATAATAGCCACTTCACAGGGA. 2125
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
562 roAsnCysIleLeuPheIleGluAsnLeuThrAlaGlnGlnTyrGlyHis 578
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
2126 .....CTCTGATCCGCTCTGTTTCAGGGTCTGACCAAGGACTT 2164
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
579 TyrPheCysGluAlaGlnGluGlySerTyr 588
      :|||: :|||: :|||: :|||: :|||: :|||: :|||:
2165 TATCACTGCTGCTACAGAAATAAGTTTC 2194
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```

seq\_name: N\_Geneseq\_36.V31121

seq\_documentation\_block:

ID V31121 standard; cDNA; 2769 BP.

AC V31121;

DT 02-SEP-1998 (first entry)

DE Human semaphorin encoding cDNA.

KW Human; semaphorin; diagnosis; nervous disease; immune disease;

KW nerve extension inhibiting activity; ds.

```

OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 61..2646
FT /tag=a
FT /product="semaphorin"
FT
PN J10155490-A.
PD 16-JUN-1998.
PF 27-NOV-1996; 332900.
PR 27-NOV-1996; JP-332900.
PA (SUMO ) SUMITOMO SEIYAKU KK.
DR WPI; 98-391044/34.
DR P-PSDB; W58340.
DR New human semaphorin gene - useful in the diagnosis of nervous system
PT and immune disorders
PS Claim 2; Page 12-13; 15pp; Japanese.
CC The present sequence encodes human semaphorin (translated from the
CC Japanese specification as semaforin). Semaphorin has nerve extension
CC inhibiting activity. The semaphorin gene is useful for the diagnosis,
CC treatment and researches on nervous diseases and immune diseases.
SQ Sequence 2769 BP; 655 A; 780 C; 738 G; 596 T;

```

alignment\_scores:

```

Quality: 591.00 Length: 695
Ratio: 1.539 Gaps: 32
Percent Similarity: 55.252 Percent Identity: 28.201

```

alignment\_block:

US-09-041-236-2 x V31121 ..

Align seg 1/1 to: V31121 from: 1 to: 2769

```

1 LeuLeuLeuLeuLeuTrpAlaAlaAlaAlaAlaAlaGlnGlyHisLeuAr 17
|||:|||||:|||||:|||||:|||||:|||||:
100 CTGGTGGTAGTGTGAGAACCGCGGTGGCATTTGCA..... 135

17 gserGlyProArgIlePheAlaValTrpLys...GlyHisValGlyGlnA 33
|||:|||||:|||||:|||||:|||||:|||||:
136 .CTGTGCTCGGCTC.....ACCTGGGAACATGGAGAGGTAGT... 174

33 spArgValAspPheGlyGlnThrGluProHisThrValLeuPheHisGlu 49
|||:|||||:|||||:|||||:|||||:|||||:
175 .....CTGGTGCAGTTTCACAAAG 192

50 ProGly.....SerSerSe 54
|||:|||||:|||||:|||||:|||||:|||||:
193 CCAGCATCTTTAAGTCTGCGCTTGTGATGAGTGGAGCAAGACAC 242

54 rValTrpValGlyArgGlyLysValTyrLeuPheAspPheProGluG 71
|||:|||||:|||||:|||||:|||||:|||||:
243 TCTGTATGTAGCGCGCGGAAGCAGTCTT..... 273

71 LyLysAsnAlaSerValArgThrValAsnIleGly..... 82
|||:|||||:|||||:|||||:|||||:|||||:
274 .....GCAGTGAATCGCTGAACATCTCTGGAAGCAACATCAG 312

83 .....SerThrLysGlySerCysLeuAspLys... 91
|||:|||||:|||||:|||||:|||||:|||||:
313 GTATATTGGAAGGTCTCTGAAGACAAAAAATCCAAGTGTGCAGAGAGGG 362

92 .....ArgAspCysGluAsnTyrIleThrLeuLeuGlu...A 103
|||:|||||:|||||:|||||:|||||:|||||:
363 GAAATCAAAAGCAGACGGAATGCTTAACACTACATTCGAGTACTACAGCCAC 412

103 rgArgSerGluGlyLeuLeuAlaCysGlyThrAsnAlaArgHisProSer 119
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413 TAAGCAGCAGCTTCCCTCTATGTGTGGGACCAATGCGTTCCAGCCACC 462

120 CysTrpAsnLeuValAsnGlyThrValValProLeuGlyGluMet.... 134
|||:|||||:|||||:|||||:|||||:|||||:
463 TGTGACCACCTGAACTTGACATCTCTCAAGTTCTTGGGAAAAGTGAAGA 512

135 ....ArgGlyTyrAlaProPheSerProAspGluAsnSerLeuValLeuP 150

```

```

513  TGGCAAGAGAGATGCCCTTCGACCCCGCCACAGCTACACATCACTCA 562
150  heGluGlyAspGluValTyrSerThrIleArgLysGlnGluTyrAsn... 165
563  TGGTGGGGCGGAGCTCTACTCT.....GGAGCTCTATAATTC 603
166  ...GlyLysIleProArgPheArgIleArgGlyGluSerGluLeuTy 181
604  TTGGCAGTGAACCATCATCTCGAAACTCTCCACACAGCTCCCTTGAG 653
181  rThrSerAspThrVal.....MetGlnAsnProGlnPheIleLysAla 196
654  GACGGAGTAGTCATCCCGTGGCTGAAGAGCCTAGTCTGCTCTCTGCT 703
196  hrIleValHisGlnAsp.....GlnAlaTyrAspAspLysIle 208
704  AGCTGATCCAGAAAGCCAGATGGTCCGGAGGGTGAAGATGACAGGTC 753
209  TyrTyrPhePheArgGluAspAsnProAspLysAsnProGluAlaPro 225
754  TACTTCTTTTTCAGGAGTATCCGTGGAGTACGAATTCGTCTCAAGTT 803
225  uAsnValSerArgValAlaGlnLeuCysArgGlyAspGlnGlyClyG 242
804  GATGATCCCGGAGTGGCAGGGTGTCAAGGGCGACCGGGCGGCTGCG 853
242  erSerLeuSerValSerLysTyrTrpAsnThrPheLeuLysAlaMet 258
854  GCATCTTGCAA...AAAAAGTGGACCTCTCTCCCTAAGGCCAGCGTG 900
259  CysSerAspAlaAlaThrAsnLysAsnPheAsnArgLeuGlnAspVal 275
901  TGCTCCAAGCCACAGACAGTGGCTGTCTTCAACATACTCTCAGGATG 950
275  eLeuLeuProAspProSerGlyGlnTrpArgAspThrArgValTyrC 292
951  TGTGCTGAGGCCCGGGC.....CTCAAGGACCTGTGTCTATCGG 994
292  alphaSer.....AsnProTrpAsnTyrSerAlaValCysValTyr 305
995  TCTTCAACCCACAGCTGAACAATGGGTGTGTGAGGGTGTGGCCCTAC 1044
306  SerLeuGlyAspIleAspLysValPhe..... 314
1045  ACATGGCCACGGTGGAGCAGTCTTCTCCGTGGAAAGTACATGCAGAG 1094
315  .....ArgThrSerSerLeuLys.....GlyTyrHisSerSerL 326
1095  TGCCACAGTGGAGCAGTCTACACCAAGTGGGTGCGGTACAATGGCC 1144
326  euProAsnProArgProGlyLysCysLeuLeu..... 339
1145  TGCCACATCCCGAGCTGGAGCGGTATGCAGACTGAGGCCCGGCGAG 1194
340  .....ProIleProThrGluThrPheGlnValAlaAs 350
1195  AACTACACGAGCTCTTCAATCTCCACAGACAAACTGCAGTTGTATA 1244
350  pArgHisProGluValAlaGlnArgValGluProMetGlyProLeuL 367
1245  AGACCACCCCTTTGATGGATGACTCAGTGACCGCAGCCGATAGACA 1291
367  hrProLeuPheHisSerLysTyrHisTyrGlnLysValAlaValHis 393
1292  CCAAGCTGATCAAAAAGATGTAACCTACACCCAGATAGGTAGACAG 1341
384  MetGlnAlaSerHisGlyGluThrPheHisValLeuTyrLeuThrAs 400
1342  ACCCAGGCCCTGGATGGGACATTTCTACGACGCTCATGTTTCATCAG 1391
400  pArgGlyThrIleHisLysValValGluProGlyGluGlnGluHisSer 417

```





```

30 aGlyGlnAspArgValasp.....PheGlyGlnThrGlu 41
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134 TGAATCCAACAATGTGATCACACCTTTCAATGGCTTGGCCAAACAGCTCCAGT 183
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42 ProHisThrValLeuPheHisGluProGlySerSerSerValTrpValGI 58
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184 TATCATACCTTCCTTTTGGATGAGAA...CGGAGTAGGCTGTATGTTGG 230
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58 yGlyArgGlyLysValTrpLeuPheAspPheProGluGlyLysAsnAlas 75
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231 AGCAAGGATCATATTTTCATTCGACCTGGTTAATATCAAGGATTTTC 280
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75 erValArgThrValAsnIleGlySerThrLys..... 85
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seq\_documentation\_block:  
Sequence 53, Application US/08835268  
Patent No. 5807826  
GENERAL INFORMATION:  
APPLICANT: Goodman, Corey S.  
APPLICANT: Kolodkin, Alex L.  
APPLICANT: Matthes, David  
APPLICANT: Bentley, David R.  
APPLICANT: O'Connor, Timothy  
TITLE OF INVENTION: The semaphorin Gene Family  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 Bush Street, Suite 3200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/835,268  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,713  
FILING DATE: 13-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: B94-002-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)343-4341  
TELEFAX: (415) 343-4342  
TELEX:  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2601 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 16..2331  
US-08-835-268-53

alignment\_scores:  
Quality: 649.50 Length: 687  
Ratio: 1.620 Gaps: 27  
Percent Similarity: 58.370 Percent Identity: 28.093

alignment\_block:

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seq\_documentation\_block:  
: Sequence 53, Application US/09060692  
: Patent No. 5935865  
: GENERAL INFORMATION:  
: APPLICANT: Goodman, Corey S.  
: APPLICANT: Kolodkin, Alex L.  
: APPLICANT: Matthes, David  
: APPLICANT: Bentley, David R.  
: APPLICANT: O'Connor, Timothy  
: TITLE OF INVENTION: The Semaphorin Gene Family  
: NUMBER OF SEQUENCES: 100  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
: STREET: 268 Bush Street, Suite 3200  
: CITY: San Francisco  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 94104  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/060,692  
: FILING DATE:  
: CLASSIFICATION: 514  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/121,713  
: FILING DATE: 13-SEP-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Osman, Richard A.  
: REGISTRATION NUMBER: 36,627  
: REFERENCE/DOCKET NUMBER: B94-002-1  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (415) 343-4341  
: TELEFAX: (415) 343-4342  
: TELEX:  
: INFORMATION FOR SEQ ID NO: 53:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 2601 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA



FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 16..2331  
 US-09-060-692-53

alignment\_scores:  
 Quality: 649.50 Length: 697  
 Ratio: 1.620 Gaps: 27  
 Percent Similarity: 58.370 Percent Identity: 28.093

alignment\_block:  
 US-09-041-235-2 x US-09-060-692-53

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; Sequence 53, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR HOBBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
PCT-US94-10151A-53

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seq\_documentation\_block:

; Sequence 1, Application US/08136922

; Patent No. 5416197

; GENERAL INFORMATION:

; APPLICANT: Raper, Jonathan A.

; APPLICANT: Luo, Yuling

; TITLE OF INVENTION: Compositions Which Regulate Neural

; REGENERATION AND METHODS OF MAKING AND USING THE SAME

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESS: No. 5416197is

; STREET: One Liberty Place

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/136,922

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

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REFERENCE/DOCKET NUMBER: UPN-1428
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 50..1480
US-09-136-922-1

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; Sequence 57, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
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APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 2854 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 451..2640
US-08-121-713D-57

alignment_scores:
Quality: 449.00 Length: 569
Ratio: 1.448 Gaps: 28
Percent Similarity: 54.482 Percent Identity: 27.592

alignment_block:
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; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 451..2640
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Quality: 449.00 Length: 569
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: Sequence 57, Application US/09060692

: Patent No. 5935865

: GENERAL INFORMATION:

: APPLICANT: Goodman, Corey S.

: APPLICANT: Kolodkin, Alex L.

: APPLICANT: Matthes, David

: APPLICANT: Bentley, David R.

: APPLICANT: O'Connor, Timothy

: TITLE OF INVENTION: The Semaphorin Gene Family

: NUMBER OF SEQUENCES: 100

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

: STREET: 268 Bush Street, Suite 3200

: CITY: San Francisco

: STATE: CA

: COUNTRY: USA

: ZIP: 94104

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent In Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/060,692

: FILING DATE:

: CLASSIFICATION: 514

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US/08/121,713

: FILING DATE: 13-SEP-1993

: ATTORNEY/AGENT INFORMATION:

: NAME: Osman, Richard A.

: REGISTRATION NUMBER: 36,627

: REFERENCE/DOCKET NUMBER: B94-002-1

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (415)343-4341

: TELEFAX: (415) 343-4342

: TELEX:

: INFORMATION FOR SEQ ID NO: 57:

: SEQUENCE CHARACTERISTICS:

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; LENGTH: 2854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
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Quality: 449.00 Length: 569
Ratio: 1.448 Gaps: 28
Percent Similarity: 54.482 Percent Identity: 27.592

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; Sequence 57, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277399 FHT UR
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
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; Sequence 63, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David R.
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 355..2493
US-08-835-268-63

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alignment_block:
US-09-041-236-2 x US-08-835-268-63 ..

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195 aThrIleValHisGlnAspGlnAlaTyrAspAspLysIleTyrTyrPheP 212

FILING DATE: 13-SEP-1994

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1851 AGACCACCATTCGGCTCGGACGCCCAACAAACCTGTGTGTCAGCATTC 1900
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1901 ACACCGTCACCTCGTATCGTCTCTGATCCAGGACGTAGTTCGCGCGAC 1950
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521 s 521
1998 G 1998
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seq_documentation_block:
; Sequence 61, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2670 base pairs
; TYPE: nucleic acid
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; TOPOLOGY: linear
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580 heCysGluAlaGlnGluCysTyrPheArgGluAlaGlnHisTyrP 596
2204 ATTGCAATTG...GGCGGCTCGCT.TTTGTGCAGCTACAACTTACAGT 2249
597 LeuLeuPro.....GluAspGlyIleMetAlaGluH1 607
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; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2670 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 268..2439
US-08-835-268-61
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418 GGAACACACGCGCAGATCATGTCGGGAGTTCACCTCGGCAAGCTGA 467
43 sThrValLeuPheHis...GluProGlySerSerValTrpValGlyG 59
468 CTATCGTACATTCATATGAACGAAGATCGAGATACGCTCTATGTGGAG 517
59 lyArgGlyLysValTyrLeuPheAspPhePro.....GluGlyLysasn 73
518 CCATGGATCGGTATTCGGTGAACCTGCAGATAATCTCCTCATCCAAT 567
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129 lPro.....LeuGlyGluMetArgGlyTyrAla.....P 139
768 GCCCGCTCGGAATATGTGATGGTGGTCTGGGCAATGCCAAGTGC 817
139 rPheSerProAspGluAsnSer..... 146
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147 .....LeuValLeuPheGluGlyAspGluValTyrSerThrIleArgL 161
918 GCGGATACGGTTATTTCCGCACTGATCTGTATAATACCTTCGGCTAAC 967
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968 GTTTSAAATATAAATTCAG.....AGGACTCTGAATATAGCAG 1005
178 SerGluLeuTyrThrSerAspThrValMetGlnAsnProGlnPheIle 194
1006 TCCAAGTGG.....TTGGACAAACCAACTTTGTGG 1037
94 sAlaThrIleValHisGlnAspGlnAlaTyrAspAspLysIleTyrP 211
1038 CTCCTTTGATATT.....GGGAGTACGTGTATTCT 1069
211 hePheArgGluAspAsnProAspLysasnProGluAlaProLeuAsnVal 227
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Date: Jan 19, 2000 12:36 AM

About: Results were produced by the GenCore software, version 4.5.  
Copyright (c) 1993-1998 CompuGen Ltd.

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-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -LOCALIGN=200 -THR SCORE=pct -ALIGN=15 -MODE=LOCAL  
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## Search information block:

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Database: EST\*  
Database sequences: 409388  
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Search time (sec): 409.410000

## score\_list:

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gb_est23:AI095332	+	715.00	1440.48	1.6e-71	469	AI095332 oyl7c05.s1 Soares sene
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VERSION AI206011.1 GI:3764683  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 459)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

On Jan 19, 1998 this sequence version replaced gi:2151569.

## CONTACT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert\_Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 2686 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 446.

## FEATURES

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trunc cDNA was constructed with a Not I and Eco RI  
double-stranded cDNA was size selected, ligated to Eco RI  
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the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library constructed by Bento Soares and  
M. Fatima Bonaldo."

BASE COUNT 87 a 134 c 151 g 87 t  
ORIGIN

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Ratio: 5.377 Gaps: 0

Percent Similarity: 98.693 Percent Identity: 98.693

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US-09-041-236-2 x AI206011

AI:7n seg 1/1 to: AI206011 from: 1 to: 459

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1 CGCGCCGCCGCTCCGCCAGGCGCACCTAAGGAGCGGCCCATCTT 50

23 eAlaValTrpIlyGlyHisValGlyGlnAspArgValAspPheGlnT 40

51 CGCGCTCTGGAAGGCCATGAGGCGAGGACCGGCTGACTTTGGCCAGA 100

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 201 CGCATCTGTGGCAGCGGTGAATATCGGCTCCACAAAGGGTCTCTGTGG 250  
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 1 (bases 1 to 476)  
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 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Jan 14, 1998 this sequence version replaced gi:1797284.

Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert\_Strausberg@nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)  
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 1. 476

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="v"  
 /clone="IMAGE:1367312"  
 /clone\_lib="NCI-CGAP\_GCB1"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 prepared from human tonsillar cells enriched for  
 germinal center B cells by flow sorting (CD20+, IgD-),  
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 primed with a Not I - oligo(dT) primer  
 [5'-TGTTACCAATCTGAAGTGGAGGGCGGCTCATTTTTTTTTTTT-  
 3']. Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT7T3 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 106 a 134 c 147 g 89 t  
 ORIGIN

alignment\_scores:  
 Quality: 791.00 Length: 159  
 Ratio: 5.006 Gaps: 0  
 Percent Similarity: 99.371 Percent Identity: 98.742

alignment\_block:  
 US-09-041-236-2 x AA827795  
 Align seg 1/1 to: AA827795 from: 1 to: 476

48 HisGluProGlySerSerValTrpValGlyGlyArgGlyLysValTy 64  
 2 CACGAGCCAGCAGCTCTCTGTGGTGGGAGGACGTGGCAAGGTCTA 51  
 64 rLeuPheAspPhePrcGluGlyLysAsnAlaSerValArgThrValAsnI 81  
 52 CCTCTTTGACTTCCCCGGGGCAAGAACGCATCTGTGGCGACGGTGAATA 101  
 81 leGlySerThrLysGlySerCysLeuAspLysArgAspCysGluAsnTyr 97  
 102 TCGGTCCACAAAGGGTCTCTGTGGATAAGCGGACTGCCGAGACTAC 151  
 98 IleThrLeuLeuGluArgSerGluGlyLeuLeuAlaCysGlyThrAs 114  
 152 ATCACTCTCTGGAGAGGGGAGTGAGGGCTGCTGGTCTGTGGCACCAC 201  
 114 nAlaArgHisProSerCysTrpAsnLeuValAsnGlyThrValProL 131  
 202 CCGCCGGCACCCAGCTGCTGGAACTTGGTGAATGGCACTGGTGGTGA. C 250  
 131 euGlyGluMetArgGlyTyrAlaProPheSerProAspGluAsnSerLeu 147  
 251 TTGGCGAGATGAGAGCTACGC. CCTTTCAGCCCGGAGAGACTCCCTG 299  
 148 ValLeuPheGluGlyAspGluValTyrSerThrIleArgLysGlnGluTy 164  
 300 GTTCTGTGTGAAGGGGACGAGGTGATTCCACCATCCGGAAGCAGGAATA 349  
 164 rAsnGlyLysIleProArgPheArgArgIleArgGlyGluSerGluLeuT 181  
 350 CAATGGGAGATCCCTCGGTTCGCCCGCATCCGGGGCGGAGAGTGTGT 399  
 181 yrThrSerAspThrValMetGlnAsnProGlnPheIleLysAlaThrIle 197  
 400 ACACCAAGTGAATCTGTATGCAACACCCACAGTTCATCAAGCCACCATC 449  
 198 ValHisGlnAspGlnAlaTyrAspAsp 206  
 450 GTGCACCAAGACGAGCTTACGATGAC 476

seq\_name: gb\_est23:AI095332

seq\_documentation\_block: 469 bp mRNA EST 24-SEP-1998  
 LOCUS AI095332 oyl7c05.sl Soares\_senescent\_fibroblasts\_NHSHF Homo sapiens CDNA  
 DEFINITION clone IMAGE:1666088 3' similar to TR:Q64906 Q64906 SIMILAR TO  
 GENBANK ACCESSION NUMBER L26081. ; mRNA sequence.

ACCESSION AI095332

NID 93434308

VERSION AI095332.1 GI:3434308

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 469)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT On Jan 19, 1998 this sequence version replaced gi:2285453.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1350

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.

Insert Length: 1645 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 468.

Location/Qualifiers

1..469

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1666088"

/clone\_lib="Soares\_senescent\_fibroblasts\_NHSHF"

/tissue\_type="senescent fibroblast"

/lab\_host="DH10B (ampicillin resistant)"

/note="Vector: pT7T3D (Pharmacia) with a modified

polylinker V.TYPE: phagemid; Site.1: Not I; Site.2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5']

TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3']

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 91 a 136 c 156 g 86 t

ORIGIN

alignment\_scores:

Quality: 715.00 Length: 156

Ratio: 4.735 Gaps: 0

Percent Similarity: 96.795 Percent Identity: 96.795

alignment\_block:

US-09-041-236-2 x AI095332

Align seg 1/1 to: AI095332 from: 1 to: 469

8 AlaaAlaAserAlaGlnGlyHisLeuArgSerGlyProArgIlePheAl 24

4 GCCCGCGCTCGCCAGCCAGCCATTAAGGACGACCCCATGCTTCGC 53

24 aValTrpLysGlyHisValGlyGlnAspArgValAspPheGlyGlnThrG 41

54 CGTCTGGAAGCCATGTAGGCGACGACCGGTGGACTTTGGCCAGACTG 103

41 luProHisThrValLeuPheHisGluProGlySerSerSerValTrpVal 57

104 AGCCGCACACGGTGTCTTTCCACGAGCCAGGAGCTCTCTGTGGGTG 153  
 58 GlyGlyAlaGlyLysValTrpLeuPheAspPheProGluGlyLysAsnAl 74  
 154 CGAGACCTGGCAAGCTTACCTCTTTGACTTCCCGGAGGCGAAGACGC 203  
 74 aserValArgThrValAsnIleGlySerThrLysGlySerCysLysLeuAspL 91  
 204 ATCTGTGCGACGGTGAATATCGGCTCCACAAAGGGTCTCTCTGGATA 253  
 91 ysArgAspCysGluAsnTrpIleThrLeuLeuGluArgSerGluGly 107  
 254 AGCGGACTGGCAGAACTACATCACTCTCTGGAGAGCGGAGTGAGGGG 303  
 108 LeuLeuAlaCysGlyThrAsnAlaArgHisProSerCysTrpAsnLeuVa 124  
 304 CTGCTGGCTGTGGACC.AACGCCGGCACCCAGCTCTCTGGAACCTGGT 352  
 124 lasnGlyThrValValProLeuGlyGluMetArgGlyTyrAlaProPheS 141  
 353 GAATGGCACTGTGTGCAT.CTTGGCGAGATGAGAGCTACGC.CCCTTCA 400  
 141 erProAspGluAsnSerLeuValLeuPheGluGlyAspGluValTrpSer 157  
 401 GCCCGGACGAGAACTCCCTGTTCTGTTTGAAGGGGACGAGGTGATTCC 450  
 158 ThrIleArgLysGlnGlu 163  
 451 CCATCCGAGACGAGAA 467

seq\_name: gb\_est21:AA968218

seq\_documentation\_block:

LOCUS AA968218 422 bp mRNA EST 19-MAY-1998

DEFINITION uh1409.r1 Soares mouse hypothalamus NMHY Mus musculus cDNA clone

IMAGE:1617929 5' similar to TR:Q64906 Q64906 SIMILAR TO GENBANK

ACCESSION NUMBER L26081. ; mRNA sequence.

ACCESSION AA968218

NID 93142111

VERSION AA968218.1 GI:3142111

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 422)

REFERENCE Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

COMMENT On Jan 17, 1998 this sequence version replaced gi:2043262.

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.

MG1:957229

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 405.

Location/Qualifiers

1..422

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="IMAGE:1617929"

FEATURES

source

/clone\_lib="Soares mouse hypothalamus NMHy"  
 /tissue\_type="hypothalamus"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGAGCGCCGCAAGGTTTTTTTTTTTTTTTTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT7T3 vector. RNA  
 provided by Dr. Wolfgang Liedtke. Library went through  
 two rounds of normalization, and was constructed by Bento  
 Soares and M. Fatima Bonaldo."  
 BASE COUNT 109 a 118 c 100 g 95 t  
 ORIGIN

alignment\_scores:  
 Quality: 705.00 Length: 140  
 Ratio: 5.222 Gaps: 0  
 Percent Similarity: 96.429 Percent Identity: 90.714

alignment\_block:  
 US-09-041-236-2 x AA968218

Align seg 1/1 to: AA968218 from: 1 to: 422

```

284 TTPAGAspThrArgValTyrglyValPheSerAsnProTrpAsnTyrsE 300
|||||
1 TGGAGATACACAGGGTCTATGGCGTTTCTCCAAACCCCTGGAACTACTC 50
|||||
300 rAlaValCysValTyrsSerLeuGlyAspIleAspLysValPheArgThrs 317
|||||
51 AGCTGTCTCGTGTATTCGCTGTGGTGTGACATTGACAGAGTCTTCGGTACT 100
|||||
317 erSerLeuLysGlyTyHisSerSerLeuProAsnProArgProGlyLys 333
|||||
101 CATCGCTCAAGGCTACACATGGCGCTTCCCAACCCCTCGACCTGGCATG 150
|||||
334 CysLeuProAspGlnGlnProIlePheGluThrPheGlnValAlaAs 350
|||||
151 TGCCTCCCAAAAGAGCCCATACCCACAGAAACCTTCAGGTAGCTGA 200
|||||
350 pArgHisProGluValAlaGlnArgValGluProMetGlyProLeuLys 367
|||||
201 TAGTCACCCAGAGGTGCTCAGAGGGTGAACCTATGGGCCACTGAAGA 250
|||||
367 hrProLeuPheHisSerLysTyHisTyrglnLysValAlaValHisArg 383
|||||
251 CACCATTTGTTCCATCTTAAGTACCATTTACCAGAAAGTGGTTCACCGC 300
|||||
384 MetGlnAlaSerHisGlyGluThrPheHisValLeuTyrlLeuThrAs 400
|||||
301 ATGCAACCCAGCAATGGAGAGACCTTCATGTGCTTTATCTAACCCAGA 350
|||||
400 pArgGlyThrIleHisLysValValGluProGlyGluGlnHisSerP 417
|||||
351 CAGGGGCACCATTCACAAAGTGGTGGGAATCAGGGGACAGGACCATAGCT 400
|||||
417 heAlaPheAsnIleMetGlu 423
|||||
401 TTGTCTTCAATATCATGGAG 420
|||||

```

seq\_name: gb\_est29:AI607683

seq\_documentation\_block:  
 LOCUS AI607683 410 bp mRNA EST 21-APR-1999  
 DEFINITION vgl1b02.y1 Soares mouse 3NME12 5 Mus musculus cDNA clone  
 IMAGE:746763 5, similar to TR:Q64906 Q64906 SIMILAR TO GENBANK  
 ACCESSION NUMBER L26081.1, mRNA sequence.  
 ACCESSION AI607683  
 NID 94616850  
 VERSION AI607683.1 GI:4616850

KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 410)  
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,T.,  
 Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,  
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
 Waterston,R. and Wilson,R.  
 TITLE The WashU-NCI Mouse EST Project 1999  
 JOURNAL Unpublished (1999)  
 COMMENT On Jun 22, 1998 this sequence version replaced gi:3246649.

Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:455747

This read is a RESEQUENCE of a previously sequenced mouse clone  
 This read has been verified (found to hit its original self in the  
 correct orientation)

Possible reversed clone: similarity on wrong strand

Seq primer: -40RP from Gibco

High quality sequence stop: 383.

Location/Qualifiers

source

1. 410  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:746763"  
 /clone\_lib="Soares mouse 3NME12 5"  
 /sex="unknown"  
 /tissue\_type="fetus"  
 /dev\_stage="12.5dpc total fetus"  
 /lab\_host="DH10B"  
 /note="Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia)  
 with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 [5' TGTACCAATCTGAAGTGGAGCGCCGCAAGGTTTTTTTTTTTTTTTTTT  
 3'], on total mouse RNA [provided by Minoru Ko, Wayne  
 State Univ.]; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT7T3 vector.  
 Library went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 94 a 126 c 99 g 89 t 2 others  
 ORIGIN

alignment\_scores:  
 Quality: 692.00 Length: 136  
 Ratio: 5.282 Gaps: 0  
 Percent Similarity: 96.324 Percent Identity: 93.382

alignment\_block:  
 US-09-041-236-2 x AI607683

Align seg 1/1 to: AI607683 from: 1 to: 410

```

214 GluAspAsnProAspLysAsnProGluAlaProLeuAsnValSerArgVa 230
|||||
3 GAAGACAACCCCTGACAGAACCAGGAGCTCTCTCAATGTGTCCGAGT 52
|||||
230 lAlaGlnLeuCysArgGlyAspGlnGlyGlyGluSerSerLeuSerValS 247
|||||
53 AGCCCCAGTTGTGCAGGGGGGACAGGGTGTGAGAGTTCTGTTCTGTCT 102
|||||

```



247 erLysTrpAsnThrPheLeuLysAlaMetLeuValCysSerAspAlaAla 263  
 103 CCAAGTGGAAACACCTTCTGAAGCCATGTGGTCTGCAGGATGCAGCC 152  
 264 ThrAsnLysAsnPheAsnArgLeuGlnAspValPheLeuLeuProAspPr 280  
 153 ACCAACAGGAACTTCATCGCTGCAGATGCTCTCTGCTCCCTGACCC 202  
 280 oSerGlyGlnTrpArgAspThrArgValTyrGlyValPheSerAsnProt 297  
 203 CAGTGGCCAGTGGAGAGATACAGGGTCTATGGGTTTCTCCAAACCCCT 252  
 297 rpAsnTyrSerAlaValCysValTyrSerLeuGlyAspIleAspLysVal 313  
 253 GGAACACTACTACGCTGCTGCGCTGATTGCTGTGGTGCATTGACAGAGTC 302  
 314 PheArgThrSerLeuLysGlyTyrHisSerLeuLeuProAsnProAr 330  
 303 TTCGTACCTCATCGCTCAAGGCTACCATGGGCTTCCCAACCCCTCG 352  
 330 gProGlyLysCysLeuProAspGlnGlnProIleProThrGluThrPheG 347  
 353 ACCGTGATGTCCTCCCAAAAGAGCAGCCCATACCCACACAAACCTTCN 402  
 347 lnValAla 349  
 403 CAGTAGCT 410

seq\_name: gb\_est7:W47265

seq\_documentation\_block: 424 bp mRNA EST  
 LOCUS W47265 424bp mRNA EST  
 DEFINITION zc39a12.r1 Soares senescent\_fibroblasts\_NBHSF Homo sapiens cDNA  
 clone IMAGE:324670 5', mRNA sequence.

ACCESSION W47265

NID 91331973

VERSION W47265.1 GI:1331973

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 424)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 731 Std Error: 0.00  
 Seq primer: mob.REGA+ET

High quality sequence stop: 394.

Location/Qualifiers

1..424

/organism="Homo sapiens"

/db\_xref="GDB:1256182"

/db\_xref="taxon:9606"

/clone="IMAGE:324670"

/clone\_lib="Soares\_senescent\_fibroblasts\_NBHSF"

/tissue\_type="senescent\_fibroblast"

/lab\_host="PH10B (ampicillin resistant)"

/note="Vector: pT73D (Pharmacia) with a modified

polylinker V\_TPE: phagemid; Site\_1: Not 1; Site\_2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
 primer [5'  
 TGTTCACCAATCGAAGTGGAGCGCCGCAATTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a cot - 5. Library constructed by Bento  
 Soares and M.Fatima Bonaldo.  
 BASE COUNT 79 a. 129 c 117 g 97 t 2 others  
 ORIGIN

alignment\_scores:

Quality: 640.00 Length: 142

Ratio: 4.706 Gaps: 1

Percent Similarity: 95.775 Percent Identity: 94.366

alignment\_block:

UC-09-041-236-2 : W47265/rev ..

Align seg 1/1 to reverse of: W47265 from: 1 to: 424

103 ArgArgSerGluGlyLeuLeuAlaCysGlyThrAsnAlaArgHisProSe 119  
 424 AGCGGAGTGTGAGGGCTGCT.GCCTGTGGCACCACCGCCGCGCAGCAG 376  
 119 rCysTrpAsnLeuValAsnGlyThrValProLeuGlyGluMetArgG 136  
 375 CTGCTGAACTGGTGANATGCACTGTGGTCCACTTGGCAGAGTGA.G 327  
 136 lyTyAlaProPheSerProAspGluAsn..SerLeuValLeuPheGluG 152  
 326 CAGACGCCCCCTTCAGCCGCGCAGAGAGACGTCGCTGCTTCTTTGAAG 277  
 152 lyAspGluValTyrSerThrIleArgLysGlnGluTyrAsnGlyLysIle 168  
 276 GGGACGAGGTGTATTCACCATCCGGAAGCAGGAATACATGGGAAGATC 227  
 169 ProArgPheArgArgIleArgGlyGluSerGluLeuTyrThrSerAspTh 185  
 226 CTCTCGTTCGCCCATCCGCGGCGAGAGTGTGTACACCATGTATAC 177  
 195 rValMetGlnAsnProGlnPheIleLysAlaThrIleValHisGlnAspG 202  
 176 TGTCATCAGACACCCACAGTTTCATCAAGCCACCATCGTGCCACCAAGAC 127  
 202 lnAlaTyrAspAspLysIleTyrTyrPhePheArgGluAspAsnProAsp 218  
 126 AGGCTTACGATGACAAGATCTACTTCTTCCGAGAGAGCAATCTCTGAC 77  
 219 LysAsnProGluAlaProLeuAsnValSerArgValAlaGlnLeuCysAr 235  
 76 AAGAACTCTGAGGCTCTCTCAATGTGTCCGCTGTGCCAGTTGTGCAG 27  
 235 gGlyAspGlnGlyGlyGluSerSer 243  
 26 GGGGAGACCGGGTGGGGAAGTTCA 2

seq\_name: gb\_est3:H02902

seq\_documentation\_block:

LOCUS H02902 446 bp mRNA EST 20-JUN-1995

DEFINITION YJ39f01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone

IMAGE:151129 3', mRNA sequence.

ACCESSION H02902

NID 9865835

VERSION H02902.1 GI:865835

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Fukuyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Futheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 446)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT

CONTACT: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1575  
 High quality sequence stops: 196  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 1575 Std Error: 0.00  
 Seq primer: Promega -2lml3  
 High quality sequence stop: 196.

FEATURES  
 source Location/Qualifiers  
 1..446  
 /organism="Homo sapiens"  
 /db\_xref="GBA:563192"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:151129"  
 /clone\_lib="Soares placenta Nb2HP"  
 /sex="Female"  
 /dev\_stage="placenta obtained at birth (full term)"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: placenta; Vector: pT7m3D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 AACTGGAGAATTCGGCGCGCAGGAATTTTTTTTTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT7m3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaudo. "  
 93 a 115 c 136 g 93 t 9 others

BASE COUNT  
 ORIGIN

alignment\_scores:  
 Quality: 633.50 Length: 150  
 Ratio: 4.728 Gaps: 3  
 Percent Similarity: 89.333 Percent Identity: 86.667

alignment\_block:  
 US-09-041-236-2 x H02902 ..

Align seg 1/1 to: H02902 from: 1 to: 446

24 AlaValTrpLysGlyHIsValGlyClnAspArgValaspPheGlyGlnTh 40  
 |||  
 1 GCCGTCTGGAAAGGCCAATGATAGGCAGGACCGGGTGGACTTTGGCCAGAC 50  
 |||  
 40 rGLuProHisThrValLeuPheHisGluProGlySerSerValTrpv 57  
 |||  
 51 TGACCCGCACACGCTGCTTTTCCACGACCCAGCAGCTCCTCTGTGTGG 100  
 |||  
 57 alGlyGlyArgGlyLysValTyrLeuPheAspPheProGluGlyLysAsn 73  
 |||  
 101 TGGGAGGACGCTGGCAAGGCTCTACCTCTTTGACTTCCCGAGGGCAAGAAC 150  
 |||  
 74 AlaSerValArgThrValAsnIleGlySerThrLysGlySerCysLeuAs 90  
 |||  
 151 GCATCTGTGCCACGGTGAATATCGGCTCCACAAGGGGTCTCTGTCTGGA 200  
 |||  
 90 pLysArgAspCysGluAsnTyrIleThrLeuGluArgSerGluG 107

3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 66 a 95 c 113 g 62 t

ORIGIN

alignment\_scores:  
Quality: 595.00 Length: 112  
Ratio: 5.360 Gaps: 0  
Percent Similarity: 99.107 Percent Identity: 97.321

alignment\_block:

US-09-041-236-2 x AA731451

Align seg 1/1 to: AA731451 from: 1 to: 336

31 GlyGlnAspArgValAspPheGlyGlnThrGluProHisThrValLeuPh 47  
|||||  
1 GGGCAGACCGGGTGGACTTTGGCCAGACTGAGCCGACACGGTGTCTTT 50  
47 eHisGluProGlySerSerValTrpValGlyGlyArgGlyLysValT 64  
|||||  
51 CCAGGAGCCAGGACCTCTCTGTGGTGGGAGACGTGCGAAGTCT 100  
64 YrLeuPheAspPheProGluGlyLysAsnAlaSerValArgThrValAsn 80  
|||||  
101 ACCTCTTTGACTTCCCGAGGGCAGAACGATCTGTGCGACACGGTGAAT 150  
81 IleGlySerThrLysGlySerCysLeuAspLysArgAspCysGluAsnTy 97  
|||||  
151 ATCGCTCCACAAAGGGTCTCTGTGGATAAGCGGGACTCGGAGAACTA 200  
97 rIleThrLeuLeuGluArgArgSerGluGlyLeuLeuAlaCysGlyThra 114  
|||||  
201 CATCACCTCTCTGGAGAGGGGAGTGTAGGGGCTGTGCGCTGTGGCACC 250  
114 snAlaArgHisProSerCysTrpAsnLeuValAsnGlyThrValValPro 130  
|||||  
251 ACGCCCGCACCCAGCTGTGGAACTGTGTAATGGCAGCTGTGTGTCGAA 300  
131 LeuGlyGluMetArgGlyTyTrAlaProPheSerPro 142  
|||||  
301 CTGCGCAGATGACAAGCTAGCGCCCTTCAAGCG 336

seq\_name: gb\_est11:AA260340

seq\_documentation\_block:  
LOCUS AA260340 347 bp mRNA EST 18-MAR-1997  
DEFINITION va91b02.r1 Soares mouse 3NME12 5 Mus musculus cDNA clone  
IMAGE:746763 5' similar to TR:G1000717 G1000717 SIMILAR TO GENBANK  
ACCESSION NUMBER L26081. ; mRNA sequence.

ACCESSION AA260340

NID 91896824

VERSION AA260340.1 GI:1896824

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 347)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le.M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT On Sep 12, 1996 this sequence version replaced gi:1400868.

Contact: Marra M/Mouse EST project

WashU-HHMI Mouse EST Project  
Washington University School  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LML: contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:455747

Possible reversed clone: similarity on wrong strand  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 296.

FEATURES  
Location/Qualifiers  
source

1..347  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:746763"  
/clone\_lib="Soares mouse 3NME12 5"  
/sex="unknown"  
/tissue\_type="fetus"  
/dev\_stage="12.5dpc total fetus"  
/lab\_host="DH10B"

/note="Organ: whole fetus; Vector: p773D-Pac (Pharmacia)  
with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5' TGTTACCAATCTGAAGTGGAGCGCCCTATTATTTTTTTTTTTT  
3'], on total mouse RNA [provided by Minoru Ko, Wayne  
State Univ.]; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified p773 vector.  
Library went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 75 a 102 c 90 g 80 t  
ORIGIN

alignment\_scores:  
Quality: 591.00 Length: 113  
Ratio: 5.277 Gaps: 0  
Percent Similarity: 99.115 Percent Identity: 96.460

alignment\_block:

US-09-041-236-2 x AA260340

Align seg 1/1 to: AA260340 from: 1 to: 347

214 GluAspAsnProAspLysAsnProGluAlaProLeuAsnValSerArgVa 230  
|||||  
3 GAAGACAACCTGACAAAGAACCCCGAGGCTCTCTCAATGTGTCCCGAGT 52  
230 LAJ31LeuCysArgGlyAspGlnGlyGlyGluSerSerLeuSerValS 247  
|||||  
53 AGCCACAGTGTGAGGGGGGACCGAGGGTGTGAGAGTTCGTGTCTCT 102  
247 erLysTrpAsnThrPheLeuLysAlaMetLeuValCysSerAspAlaAla 263  
|||||  
103 CCAGTGGAAACACCTCTCTGAAAGCCATGTGGTCTCAGGATGCAGCC 152  
264 ThrAsnLysAsnPheAsnArgLeuGlnAspValPheLeuLeuProAspPr 280  
|||||  
53 ACCAACAGGAACCTCAATCGCTGCAAGATGTCTTCCTGCTCCCTGACCC 202  
280 cSerGlyGlnTrpArgAspThrArgValTyGlyValPheSerAsnProT 297  
|||||  
203 CAGTGGCCAGTGGAGAGATACCGAGGGTCTATGGCGTTTCTTCCAACCCCT 252  
297 rPasnTySerAlaValCysValTySerLeuGlyAspLeuAspLysVal 313  
|||||  
255 GGAAGTACTCAGCTGTCTGCTGTATTTCGCTGTGTGATGCAGAGATC 302  
314 PheArgThrSerSerLeuLysGlyTyTrHisSerSerLeu 326  
|||||



FEATURES	source
High quality sequence stop: 323.	
Location/Qualifiers	
1. .549	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/map="12p"	
/clone="IMAGE:746763"	
/clone_lib="Soares mouse 3NME12 5"	
/sex="unknown"	
/tissue_type="fetus"	
/dev_stage="12.5dpc total fetus"	
/lab_host="DH10B"	
/note="Organ: whole fetus; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTCGAGTGGGAGCGGCCGCTTATTTTTTTTTTTTTTT 3'], on total mouse RNA [provided by Minoru KO, Wayne State Univ.]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."	
102 a	146 c 155 g 144 t 2 others
BASE COUNT	
ORIGIN	

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alignment_scores:
  Quality: 572.50      Length: 159
  Ratio: 4.241         Gaps: 8
  Percent Similarity: 84.906      Percent Identity: 72.956

alignment_block:
  US-09-041-236-2 x AI662727/rev ..
  Align seg 1/1 to reverse of: AI662727 from: 1 to: 549

452 GluValSerGlnValProLeuAspLeuCysGluValTyrGlyGly.GlyC 468

```

495 GAAGTGCACGAGCC...CTGGACATGTGTAGGTTTCAGCGGGGGCTGCAT 449

488 yshHisGlyCysLeuMetSer.ArgaspProTyrCysGlyTrpAspGlnGI 484

[illegible][illegible]

Align seg 1/1 to: AA856724 from: 1 to: 332

```

36 AspPheGlyGlnThrGluProHisThrValLeuPheHisGluProGlySer 52
|||||
2 GACTTTGGCCAGACTGAGCCGCACACAGGTGCTTTTCCACGAGCAGCAG 51
|||||
52 rSerSerValTyrValGlyGlyArgGlyLysValTyrLeuPheAspPheP 69
|||||
52 CTCTCTGCTGGTGGGAGAGAGTGGCAGAGTCTACCTCTTTGACTTCC 101
|||||
69 roGluGlyLysAsnAlaSerValArgThrValAsnIleGlySerThrLys 85
|||||
102 CCGAGGCAAGAACGCATCTGTGGCAGCGTGAATATCGGCTCCACAAAG 151
|||||
86 GlySerCysLeuAspLysArgAspCysGluAsnTyrIleThrLeuLeuG 102
|||||
152 GGTCTCTGTGGATAGCGGGAGTGGGAGAACTACATCATCTCTCTGGA 201
|||||
102 uArgArgSerGluGlyLeuLeuAlaCysGlyThrAsnAlaArgHisPro 119
|||||
202 GAGCGGAGTGGGGGCTGTGGCTGTGGCACCACGACGACGCCCA 251
|||||
119 erCysTrpAsnLeuValAsnGlyThrValValProLeuGlyGluMetArg 135
|||||
252 GCTGCTGGAACCTGGTGAATGGCACTGTGTGCA.CTTGGCGAGATGAGA 300
|||||
136 GlyTyrAlaProPheSerProAspGluAsnSer 146
|||||
301 GGCTACGC.CCCTTCAGCCCGGACGAGAACTCC 332

```

seq\_name: gb\_est3:R33537

seq\_documentation\_block: 344 bp mRNA EST 28-APR-1995  
LOCUS YH79d03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone  
DEFINITION IMAGE:135941 5' similar to SP:VA39\_VACC P21062 PROTEIN ;, mRNA  
sequence.

ACCESSION R33537

NID 9789395

VERSION R33537.1 GI:789395

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

AUTHORS Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 344)

Hillier, L., Clark, N., Duboue, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1078

High quality sequence stops: 275

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Insert Length: 1078 Std Error: 0.00

Seq primer: W13RP1

High quality sequence stop: 275.

Location/Qualifiers

1..344

/organism="Homo sapiens"

FEATURES

source

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/db_xref="GDB:541932"
/db_xref="taxon:9606"
/clone="IMAGE:135941"
/clone_lib="Soares placenta Nb2HP"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AATGGAAGAATTCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
BASE COUNT 74 a 87 c 106 g 75 t 2 others
ORIGIN

```

alignment\_scores:  
Quality: 550.00 Length: 117  
Ratio: 4.911 Gaps: 4  
Percent Similarity: 95.726 Percent Identity: 94.872

alignment\_block:

US-09-041-236-2 x R33537/rev

Align seg 1/1 to reverse of: R33537 from: 1 to: 344

227 ValSerArgValAlaGlnLeuCysArgGly.AspGlnGlyGlyGlySerS 243

|||||

344 GTGTCCCGTGTGCCNAATTGTCAAGGGNGGACAGGGTGGGAAAGTT 295

|||||

243 erLeuSerValSer.LystrpAsnThrPheLeu.LysAlaMetLeuVal. 258

|||||

294 CACTGTCACTCTCCAAGTGAACACTTTTCTGAAAGCCACTGCTGGTAA 245

|||||

259 CysSerAspAlaAlaThrAsnLysAsnPheAsnArgLeuGlnAspValP 275

|||||

244 TGCAGTGTGCTGCCACCAAGAACTTCAACAGGCTGCAAGACGCTCT 195

|||||

275 eLeuLeuProAspProSerGlyGlnTrpArgAspThrArgValTyrGlyV 292

|||||

194 CTGTCTCCCTGACCCAGCGCCAGTGGAGGACACACAGGGTCTATGGTG 145

|||||

292 alphaSerAsnProTrpAsnTyrSerAlaValCysValTyrSerLeuGly 308

|||||

144 TTTTCTCCAACCCCTGGAACACTACTCAGCCGCTGTGTGTATTCCCTCGGT 95

|||||

309 AspIleAspLysValPheArgThrSerSerLeuLysGlyTyrHisSerSe 325

|||||

94 GACATTGACAAGGTCTTCGTCACCTCTCTCCTCAAGGGCTACCACTCAAG 45

|||||

325 rLeuProAsnProArgProGlyLysCysLeuProAspGlnGln 339

|||||

44 CTTTCCCAACCCCGCGCCCTGGCAAGTGCCTCCAGACGACGAG 2

|||||

seq\_name: gb\_est3:R33439

seq\_documentation\_block:

LOCUS R33439 309 bp mRNA EST 28-APR-1995

DEFINITION YH79d03.s1 Soares placenta Nb2HP Homo sapiens cDNA clone

IMAGE:135941 3', mRNA sequence.

ACCESSION R33439

NID 9789297

VERSION R33439.1 GI:789297

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 309)



```
314 Phe.....ArgThr.....Serse 318
    |||      |||||
157 TTCTCTGGGAGCTATAGGACCTTCGACATGGAGATGCACCAGTGGAGTTC 206
    |||
318 rLeuLysGlyTyrHisSerSerLeuProAsnProArgProGlyLysCysL 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
207 ACTGCTGGGAAACACTCGTACCTG.....GGACAGTGTG 241
    |||
335 euProAspGlnGlnProIleProThrGluThrPheGlnValAlaAspArg 351
    |||
242 GACTGGAC.....AAAGCCACCGATTCA 264
    |||
352 HisProGluValAlaGlnArg.....ValGluPr 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
265 GAGCTAGAGGAGGTGAAGAGGAGTTCCTGACCAGTGGTGGAGTCAAAACC 314
    |||
361 oMet.....GlyProLeuLysThrProLeuPheHisSerLysTyrHisT 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
315 TGTGGCAGACGGTCCAGTG.....GTTGTTTCTCTGAGCATCAGT 355
    |||
376 yGlnLysValAlaValHisArgMetGlnAlaSerHisGlyGluThrPhe 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
356 ACAGTCGTGTGGTGGCGATGAGCAGCAGCAGCAACGCGCAACAGTAC 405
    |||
393 HisValLeuTyrLeuThrThrAspArgGlyThrIleHisLysValVal.. 408
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
406 ACCGTCCTTTTCTGCNCACAGAGTCTGGATTCTCTGCACAAGATTGTTGT 455
    |||
409 ....GluProGlyGluGlnGluHisSerPheAlaPheAsnIleMetGluI 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
456 TCTGGATTGGGT.....GCCCTGGTCATTGAGGAGA 487
    |||
424 leGlnProPheArgArgAlaAlaIleGlnThrMetSerLeuAspAla 440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
488 TTCAGGTCCTTCACAGCCACACAGCTGCTGAGAGCATCGTCTCTCGACC 537
    |||
441 GluArgGlyLysLeuTyrValSerSerGlnTrpGluValSerGlnValPr 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
538 ACCAGGGGGCAGTATACNGGGAACGCTGAGGGGTGTCACCTCCGTCGCC 587
    |||
457 oLeuAspLeuCysGluValTyrGlyGlyCysHisGlyCysLeuMets 474
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
588 TGTGGCGAACTGCTCCGTTTAC...AGAAGCTCGGTCTAGTGTGTTCTGG 634
    |||
474 exArgAspProTyrCysGlyTyrAspGlnGlyArg.....CysIleSer 488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
635 CCAGAGATCCTCTGTGTGGTGGAGTCCGACAGGAGGGAGTGCACAAT 684
    |||
489 IleTyrSerSerGluArgSerValLeuGlnSerIleAsnProAlaGluPr 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
685 CTGACACAGGATCGNGACACATAGNTCAGGATGTGGA..... 723
    |||
505 oHisLysGluCysProAsnProLysProAspLysAlaProLeuGlnLysV 522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
724 .....AATGGAAATATAGAAAAGCATGTCTACAAACAA 757
    |||
522 aISer 523
    |||
758 TCAGT 762
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